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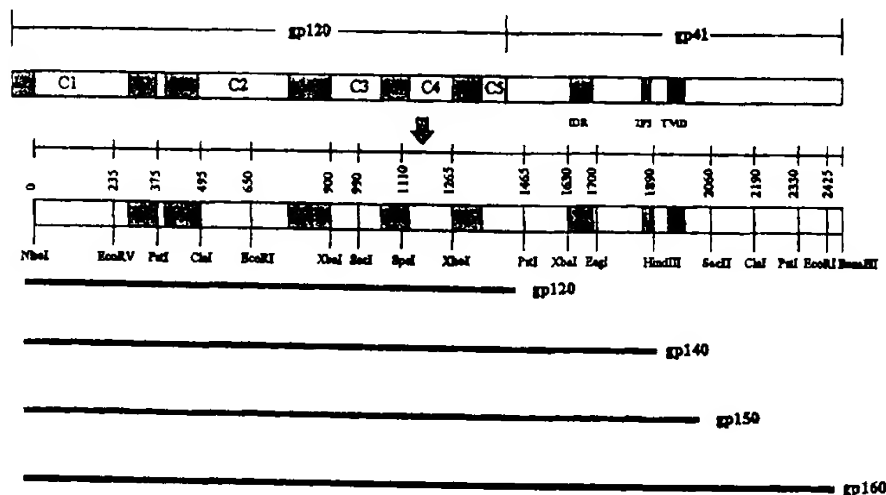
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(54) Title: METHOD FOR PRODUCING A NUCLEOTIDE CONSTRUCT WITH OPTIMISED CODONS FOR AN HIV GENETIC VACCINE BASED ON A PRIMARY, EARLY HIV ISOLATE AND SYNTHETIC ENVELOPE BX08 CONSTRUCTS

Synthetic BX08 Env
Strategy for building the full-length gp160 and derived truncated forms

**(57) Abstract**

The present invention relates to a method for producing a nucleotide sequence construct with optimized codons for an HIV genetic vaccine based on a primary, early HIV isolate. Specific such nucleotide sequence construct are the synthetic envelope BX08 constructs. The invention further relates to the medical use of such constructs for the treatment and prophylaxis of HIV through DNA vaccine and for diagnostics.

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Method for producing a nucleotide sequence construct with optimised codons for an HIV genetic vaccine based on a primary, early HIV isolate and synthetic envelope BX08 constructs.

5 Field of the invention

The invention relates to a DNA vaccine against HIV, which is designed from a clinical primary isolate. One aspect of the invention relates to a method of producing a nucleotide sequence construct, in a preferred aspect based on a cassette system, the nucleotide sequence construct being used as a DNA vaccine. The method can, for example, lead to the
10 disclosed synthetic BX08 HIV-1 envelope vaccine nucleotide sequence construct, designed to generate suitable DNA vaccines against HIV, specifically HIV-1. Furthermore, the invention can be used for the production of recombinant protein antigens.

Background of the invention

15 There is an urgent need for new vaccine strategies against HIV. One such new promising strategy is called genetic immunisation or DNA vaccine (Webster et al 1997). Some of the advantages of a DNA vaccine against HIV is the induction of Th cell activation, induction of antibodies also against conformational dependent epitopes, and the induction of cellular immunity. So far, most DNA vaccine envelope genes tried, have been from tissue culture
20 adapted virus strains (Boyer et al 1997) that often differs in several aspects from primary clinical isolates (such as early isolates) e.g. in co-receptor usage (Choe et al 1996, Dragic et al 1997).

One disadvantage in HIV envelope based DNA vaccines may be the intrinsic relatively low
25 expression which is regulated by the Rev expression. This may prevent an optimal investigation of the vaccines in small animal models like mice where Rev is functioning suboptimally. Recently it has been shown using the tissue culture adapted HIV-1 MN strain, that an exchange of the HIV codon usage to that of highly expressed mammalian genes greatly improves the expression in mammalian cell lines and renders the HIV expression Rev
30 independent (Haas et al 1996). Additionally, it is known that rare codons cause pausing of the ribosome, which leads to a failure in completing the nascent polypeptide chain and a uncoupling of transcription and translation. Pausing of the ribosome is thought to lead to exposure of the 3' end of the mRNA to cellular ribonucleases.

The world-wide spread of HIV-1 has presently resulted in 8,500 new infections daily and AIDS is now the number 1 cause of death among US males (and number 3 among US females) aged 25-40 years. The epidemic hot-spots now include Eastern Europe, India and South East Asia and southern Africa. The attempts to solve this world-wide problem involve education, prevention, treatment and vaccine development. Affordable protective vaccines represent the best solution to the world-wide problem of infection with HIV-1. Induction of virus neutralising antibodies is one of the key components in vaccine development. Several recombinant envelope vaccines have been tested in humans and animals, however, they seem unable to induce sufficient protection. In this respect DNA vaccination may provide a different and more natural mode of antigen presentation. It is hoped that the immune responses induced by such DNA vaccines could aid in limiting virus replication, slowing disease progression or preventing occurrence of disease. Unfortunately many HIV envelope vaccines induce only moderate levels of antibodies. This could in part be due to limitations in expression, influenced by regulation by the Rev protein and by a species-specific and biased HIV codon usage. Also the virus variability is considered a barrier for development of antibody based vaccines and thus a tool for more easy producing of closely related vaccine variants is needed.

It has been suggested to improve the immunogenicity and antigenicity of epitopes by certain mutations in the envelope gene. An elimination of certain immune dominant epitopes (like V3) could render less immune dominant but more relevant, conserved, or hidden epitopes more immunogenic (Bryder et al 1999). Also elimination of certain N-linked glycosylation sites could improve the exposure of relevant epitopes and increase the immunogenicity of those epitopes. Thus, it is possible that elimination of the glycosylation sites in V1 and V2 may in a more favourable way expose neutralising epitopes (Kwong et al 1998, Wyatt et al 1998). The HIV envelope contains putative internalisation sequences in the intracellular part of gp41 (Sauter et al 1996). Thus it would be relevant to eliminate and/or mutate the internalisation signals in a membrane bound HIV envelope vaccine gene to increase the amount of surface exposed vaccine derived HIV glycoproteins as gp150. Since the antibody response, that is measured and calculated in titers, is improved by adding the secreted gp120 as opposed to adding the membrane bound form (Vinner et al 1999), it could be advantageous to express the vaccine as a secreted gp120 or a secreted gp140. This would include important parts of gp41, such as the 2F5 neutralising linear epitope (Mascola et al 1997).

Summary of the invention

Our suggested solution to the problems described above is to design DNA envelope vaccines from a clinical primary isolate with Rev-independent high expression in mammals, that is built as a cassette for easy variant vaccine production.

5

A method of producing a nucleotide sequence construct with codons from highly expressed mammalian proteins based on a cassette system coding for an early, primary HIV envelope is described. The method comprises the steps of direct cloning of an HIV gene, derived from a patient within the first 12 months of infection, thereby obtaining a first nucleotide sequence; 10 designing a second nucleotide sequence utilising the most frequent codons from mammalian highly expressed proteins to encode the same amino acid sequence as the first nucleotide sequence; redesigning the second nucleotide sequence so that restriction enzyme sites surround the regions of the nucleotide sequence encoding functional regions of the amino acid sequence and so that selected restriction enzyme sites are removed, thereby obtaining 15 a third nucleotide sequence encoding the same amino acid sequence as the first and the second nucleotide sequence; redesigning the third nucleotide sequence so that the terminals contain convenient restriction enzyme sites for cloning into an expression vehicle; producing snuts between restriction enzyme sites as well as terminal snuts and introducing snuts into an expression vehicle by ligation. The nucleotide sequence construct obtained by this 20 method uses the mammalian highly expressed codons (figure 1) and renders the envelope gene expression Rev independent and allows easy cassette exchange of regions surrounded by restriction enzyme sites that are important for immunogenicity, function, and expression.

25 The method can, for example, lead to the disclosed synthetic, Rev-independent, clinical (such as early), primary HIV-1 envelope vaccine gene, built as a multi cassette. From the sequence of the envelope of the HIV-1 BX08 isolate (personal communication from Marc Girard, Institute Pasteur, Paris), the present inventors have designed a synthetic BX08 HIV-1 envelope vaccine nucleotide sequence construct.

30

With the great diversity of envelopes in HIV among different patients and within one patient, it would be of advantage to vaccinate with several envelope variants, all being highly expressed. To avoid synthesising several full length envelopes, it is much easier to exchange relevant parts of an envelope cassette to various strains in a multivalent vaccine

35

Whether it is the disclosed synthetic BX08 nucleotide sequence construct, or any of the nucleotide sequence constructs obtained by the method, they are designed to generate suitable DNA vaccines against HIV, specifically HIV-1. In this case the mammal, preferably a human being, is inoculated with the nucleotide sequence construct in an expression vehicle
5 and constitutes a host for the transcription and translation of the nucleotide sequence construct. The nucleotide sequence constructs of the present invention can furthermore be used for the production of recombinant protein antigens. In this case the nucleotide sequence construct is placed in an expression vehicle and introduced into a system (e.g. a cell-line), allowing production of a recombinant protein with the same amino acid sequence.
10 The recombinant protein is then isolated and administered to the mammal, preferably a human being. The immune system of the mammal will then direct antibodies against epitopes on the recombinant protein. The mammal, preferably a human being, can thus be primed or boosted with DNA and/or recombinant protein obtained by the method of the invention.

15

A relevant HIV DNA vaccine can potentially be used not only as a prophylactic vaccine, but also as a therapeutic vaccine in HIV infected patients, e.g. during antiviral therapy. An HIV specific DNA vaccine will have the possibility to induce or re-induce the wanted specific immunity and help the antiviral therapy in limiting or even eliminating the HIV infection. The
20 immunogenicity and antigenicity of epitopes in the envelope can be improved by certain mutations in the envelope gene. The cassette system allows for easy access to the relevant parts of the envelope gene, and thereby eased efforts in the process of genetic manipulation. Some suggested mutations are: an elimination of certain immune dominant epitopes (like V3); elimination of certain N-linked glycosylation sites (like glycosylation sites around V2);
25 elimination and/or mutation of the nucleotide sequence encoding the internalisation signals in the cytoplasmic part of a membrane bound HIV envelope to increase the amount of surface exposed vaccine derived HIV glycoproteins; elimination or mutation of the cleavage site between gp120 and gp41; with introduced mutations in gp41 for preserving conformational epitopes.

30

Table 1 below, lists the nucleotide sequence constructs of the invention by the names used herein, as well as by reference to relevant SEQ ID NOs of DNA sequences, and the amino acid sequence encoded by the DNA sequence in the preferred reading frame. It should be noted, that the snut name consist of the number of the approximate position for the end of
35 the snut and the restriction enzyme used to cleave and/or ligate that end of the snut.

Table 1 List of names of nucleotide sequence constructs (Snuts (S) and Pieces (P)) with reference to SEQ ID NO for the nucleotide sequence and protein sequence.

Name	Nucleotide SEQ ID NO:	Protein SEQ ID NO:
S ₀ -N-Lang	1	2
S ₂₃₅ EcoRV	3	4
S ₃₇₅ PstI	5	6
S ₄₉₅ Clal	7	8
S ₆₅₀₋₇₂₀ EcoRI	9	10
S ₉₀₀ XbaI	11	12
S ₉₉₀ SacI	13	14
S ₁₁₁₀ SpeI	15	16
S ₁₂₆₅ XhoI	17	18
S _{1265gp120}	19	20
S _{1265gp160}	21	22
S ₁₄₆₅ PstI	23	24
S ₁₄₆₅ PstI cys	25	26
S ₁₆₃₀ XbaI	27	28
S ₁₇₀₀ EagI	29	30
S ₁₈₉₀ HindIII	31	32
S ₂₀₆₀ SacII	33	34
S ₂₁₉₀ Clal	35	36
S ₂₃₃₀ PstI	37	38
S ₂₄₂₅ ES	39	40
P ₁	41	42
P ₂	43	44
P ₃	45	46
P _{3GV1}	47	48
P _{3GV1V2}	49	50
P _{3GV2}	51	52
P _{4gp160}	53	54
P _{4gp150}	55	56
P _{4gp140}	57	58
P ₅	59	60
P _{8gp160}	61	62
P _{8gp150}	63	64
P _{8gp140}	65	66
synBX08-140	67	68
synBX08-150	69	70
synBX08-160	71	72
synBX08-120	73	74
synBX08-41	75	76

Detailed disclosure of the invention

One aspect of the present invention relates to a method for producing a nucleotide sequence construct coding for an HIV gene. The nucleotide sequence construct is produced as a cassette system consisting of snuts. A snut (S) is a nucleotide sequences construct between
5 restriction enzyme cleavage sites comprising the minimal entity of the cassette system.

First an HIV gene is obtained from a patient within the first 12 months of infection. The term HIV should be understood in the broadest sense and include HIV 1 and HIV 2. It is possible to determine the period in which the infection has taken place with an accuracy depending
10 on the frequency of the blood tests taken from the patient. For example, patients suffering from various diseases such as lack of certain factors in their blood or hepatitis have their blood tested on a regular basis making it possible to determine the period in which the infection has taken place. Apart from patients with diseases wherein blood tests are used to monitor the course of the disease, other groups of patients have blood tests taken, e.g. blood
15 donors. Unfortunately, humans are still infected due to transfer of virus in blood samples, medical equipment, etc., making it possible to determine the date where the infection has taken place within the time frame of a few days. The importance of obtaining the virus early in the course of the infection is due to the known fact that many early isolates share the common feature of staying relatively constant in their envelope sequences (Karlsson et al.,
20 1998). As these early isolates may share cross-reactive antibody- and/or T-cell epitopes a vaccine based on such early isolates would have a better chance of inducing immune response to shared epitopes of the virus. It is believed that an early, directly cloned virus isolate will share immunogenic sites with other early virus isolates seen during an HIV infection, so that if a mammal generates antibodies and/or T-cells directed against these
25 epitopes, the transferred virus will be eliminated prior to the extensive mutations that may occur after approximately 12 months of infection. Thus, the virus should be isolated as early as possible, that is within the first 12 months of infection, such as 11, 10, 9, 8, 7, 6, 5, 4, 3, 2, 1, or 0.5 month after infection.

30 The HIV gene for genetic vaccine is preferably cloned directly from viral RNA or from proviral DNA. Direct cloning in this application stands for the virus not being multiplied in stable cell lines *in vitro*. It is presently expected that passing the virus through a stable cell line will promote mutation in the virus gene. It is particularly preferred not to pass the virus through cells lines selecting for viruses with CXCR4 receptor usage. Direct cloning also includes
35 multiplication of virus in e.g. PBMC (peripheral blood mononuclear cells) since all virus can

multiply in PBMC, and this type of multiplication generally does not select for CXCR4 receptor usage. Multiplication of virus is often necessary prior to cloning. Preferably cloning is performed directly on samples from the patient. In one embodiment of the invention, cloning is performed from patient serum. The cloning is then performed directly on the HIV
5 virus, that is on RNA. In another embodiment of the invention cloning, is performed from infected cells. The cloning is then performed on HIV virus incorporated in the genes in an infected cell (e.g. a lymphocyte), that is on DNA. In the latter case the virus might be a silent virus, that is a non-replicating virus. To evaluate if the virus is silent, capability of multiplication in e.g. PBMC is tested.

10

Cloning is a technique well known to a person skilled in the art. A first nucleotide sequence is hereby obtained. In another aspect of the invention, the first nucleotide sequence, sharing the properties mentioned with direct cloning, is obtained by other means. This could be from a database of primary isolates or the like.

15

Based on the first nucleotide sequence, the amino acid sequence encoded by said nucleotide sequence is determined. A second nucleotide sequence encoding the same amino acid sequence is then designed utilising the most frequent codons from highly expressed proteins in mammals (e.g. figure 1 presenting the most frequent codons from
20 highly expressed proteins in humans).

Presently, it appears that the usage of the most frequent codons from mammalian highly expressed proteins has two advantages: 1) the expression is Rev independent; 2) the level of expression is high. The Rev independence is especially advantageous when performing
25 experiments in mice where the Rev systems is functioning sub-optimally. For the use in human vaccine, Rev independence and high expression are important to increase the amount of antigen produced. The determination of the codons for high expression is in this context based on the statistics from human highly expressed proteins (Haas, Park and Seed, 1996 hereby incorporated by reference). It is contemplated that the expression of a protein
30 can be even higher, when current research in binding between codon (on the mRNA) and anticodon (on the tRNA) reveals codons with optimal binding capabilities, and when interactions in-between codons and/or in-between anticodons are known.

The second nucleotide sequence designed utilising optimised codons is then redesigned to
35 obtain a third nucleotide sequence. The purpose of the redesigning is to create unique restriction enzyme sites around the nucleotide sequence encoding functional regions of the

- amino acid sequence. By having unique restriction enzyme sites around the nucleotide sequence encoding functional regions of the amino acid sequence, the nucleotide sequence encoding functional regions of the amino acid sequence can easily be isolated, changed, and re-inserted. Examples of functional regions of the amino acid sequence are transmembrane
- 5 spanning regions, immunodominant regions, regions with antibody cross reacting domains, fusion domains and other regions important for immunogenicity and expression such as variable region 1 (V1), variable region 2 (V2), variable region 3 (V3), variable region 4 (V4) and variable region 5 (V5).
- 10 It is important to select the restriction enzymes sites with care. By changing the second nucleotide sequence to insert restriction enzyme sites around the nucleotide sequence encoding functional regions of the amino acid sequence, the third nucleotide sequence must still code for the same amino acid sequence as the second and first nucleotide sequence do. Thus, if necessary, the second nucleotide sequence is redesigned by changing from
- 15 optimised codons to less optimal codons. It is understood, that the restriction enzyme sites around the nucleotide sequence encoding functional regions of the amino acid sequence should preferably be placed in the terminal region of the nucleotide sequence encoding functional regions of the amino acid sequence. That is preferably outside the nucleotide sequence encoding functional regions of the amino acid sequence, such as 90 nucleotides
- 20 away, e.g. 81, 72, 63, 54, 45, 36, 27, 21, 18, 15, 12, 9, 6, 3 nucleotides away, but could also be inside the nucleotide sequence encoding functional regions of the amino acid sequence, such as 54, 45, 36, 27, 21, 18, 15, 12, 9, 6, 3 nucleotides inside the nucleotide sequence encoding the functional region of the amino acid sequence.
- 25 The type of restriction enzyme sites allowed is determined by the choice of expression vector. In certain cases, the number of restriction enzyme sites is limited and it is hard, if not impossible, to place unique restriction enzyme sites around all the nucleotide sequences coding for functional regions of the amino acid sequence. This problem can be solved by dividing the entire nucleotide sequence into pieces, so that each piece comprises only
- 30 unique restriction enzyme sites. Modifications to each of the piece is performed separately prior to assembly of the pieces. It is preferred that the nucleotide sequence is divided into 9 pieces. In another aspect, the nucleotide sequence is divided into 8 pieces, or 7, or 6, or 5, or 4, or 3, or 2 pieces. It is especially preferred that the nucleotide sequence is divided into 3 pieces.

Thus, the redesign of the second nucleotide sequence is an interaction between the choice of cloning vector, expression vector, selection of restriction enzyme sites, dividing into pieces, and exchange of codons to insert restriction enzyme sites. In a preferred embodiment of the present invention the cloning vector is Bluescript allowing the restriction enzyme sites chosen from the group consisting of: *EagI*, *MluI*, *EcoRV*, *PstI*, *Clal*, *EcoRI*,
5 *XbaI*, *SacI*, *SpeI*, *XhoI*, *HindIII*, *SacII*, *NotI*, *BamHI*, *SmaI*, *Sall*, *DraI*, *KpnI*. If other cloning vectors are chosen, other restriction enzyme sites will be available as known by the person skilled in the art.

- 10 As a part of the redesigning of the second nucleotide sequence, selected restriction enzyme sites may be removed. The selected restriction enzyme sites to be removed are those sites that are sites of the same type as the ones already chosen above and that are placed within the same piece. The removal of these restriction enzyme sites is performed by changing from optimised codons to less optimal codons, maintaining codons for the same amino acid
15 sequence.

The third nucleotide sequence is redesigned so that the terminal snuts contain convenient restriction enzyme sites for cloning into an expression vehicle. The expression "vehicle" means any nucleotide molecule e.g. a DNA molecule, derived e.g. from a plasmid,
20 bacteriophage, or mammalian or insect virus, into which fragments of nucleic acid may be inserted or cloned. An expression vehicle will contain one or more unique restriction enzyme sites and may be capable of autonomous replication in a defined host or vehicle organism such that the cloned sequence is produced. The expression vehicle is an autonomous element capable of directing the synthesis of a protein. Examples of expression vehicles are
25 mammalian plasmids and viruses, tag containing vectors and viral vectors such as adenovirus, vaccinia ankara, adenoassociated virus, canarypox virus, simliki forest virus (sfv), Modified Vaccinia Virus Ankara (MVA), and simbis virus. In one embodiment of the invention, the expression vector contains tag sequences. In another embodiment of the invention a bacteria is transformed with an expression plasmid vector and the bacteria is
30 then delivered to the patient. Preferred expression vehicles are simliki forest virus (sfv), adenovirus and Modified Vaccinia Virus Ankara (MVA).

The snuts are produced by techniques well known by the person skilled in the art. The preferred method for synthesising snuts, is herein referred to as "the minigene approach"
35 wherein complementary nucleotide strands are synthesised with specific overhanging sequences for annealing and subsequent ligation into a vector. This can be performed with

two sets of complementary nucleotide strands, or with three sets of complementary nucleotide strands. The minigene approach minimises the known PCR errors of mismatches and/or deletions, which may occur due to hairpins in a GC rich gene with mammalian highly expressed codons. In figures 10-21, the production of a representative selection of snuts is
5 illustrated.

For the production of long snuts, that is snuts of more than about 240 nucleotides, the technique of overlapping PCR is preferred as illustrated in figure 8. Herein two nucleotide strands about 130 nucleotides long with an overlap are filled to obtain a double strand, which
10 is subsequently amplified by PCR.

For the production of multiple snuts with a length of less than about 210 nucleotides, one preferred technique is normal PCR. In a preferred production technique the snuts are synthesised with the same 5' flanking sequences and with the same 3' flanking sequences,
15 as illustrated in figure 9. The advantages of this approach is, that the same PCR primer set can be used for amplification of several different snuts.

As known by the person skilled in the art, special conditions have to be used for each individual PCR reaction and it should be optimised to avoid inherent problems like deletions
20 mismatches when amplifying GC rich genes from synthetic ssDNA material. Whichever of the above mentioned techniques are used, it is well known by the person skilled in the art, that it will be necessary to correct unavoidable mismatches produced either due to the nucleotide strand synthesis material and/or the PCR reaction. This can be performed by site directed mutagenesis techniques.

25

After the various snuts have been produced, they are assembled into pieces and subsequently into the complete gene. Methods for assembly (such as ligation) are well known by the person skilled in the art.

30

In a preferred embodiment of the present invention the HIV gene encodes the entire HIV envelope. It is understood that the HIV envelope can be the full length envelope gp160 as well as shorter versions such as gp150, gp140, and gp120 with or without parts of gp41

35 As will be known by the person skilled in the art, the HIV is divided into several groups. These groups presently include group M, group O, and group N. Further, the HIV is divided

into subtypes A, B, C, D, E, F, G, H, I, and J. In the present invention subtype B is preferred due to the high prevalence of this subtype in the Western countries.

The determination of groups and subtypes is based on the degree of nucleotide sequence identity in the envelope gene is presently defined as follows: If the sequence identity is more than 90% the viruses belong to the same subtype; if the sequence identity is between 80% and 90% the viruses belong to the same group. If the sequence identity is less than 80% the viruses are considered as belonging to different groups.

- 10 One aspect of the invention relates to a nucleotide sequence construct in isolated form which has a nucleotide sequence with the general formula (I), (II), (III), or (IV)

(I) $P_1-S_{495C1a1}-S_{650-720EcoRI}-P_2-S_{1265gp120}$

(II) $P_1-S_{495C1a1}-S_{650-720EcoRI}-P_2-S_{1265XhoI}-S_{1465PstII}-P_{4gp140}$

(III) $P_1-S_{495C1a1}-S_{650-720EcoRI}-P_2-S_{1265XhoI}-S_{1465PstII}-P_{4gp150}$

- 15 (IV) $P_1-S_{495C1a1}-S_{650-720EcoRI}-P_2-S_{1265XhoI}-S_{1465PstII}-P_{4gp160}-S_{2060SacII}-P_5$

wherein P_1 designates the nucleotide sequence SEQ ID NO:41, a nucleotide sequence complementary thereto, or a nucleotide sequence with a sequence identity of at least 90% thereto;

wherein $S_{495C1a1}$ designates the nucleotide sequence SEQ ID NO: 7, a nucleotide sequence complementary thereto, or a nucleotide sequence with a sequence identity of at least 95% thereto;

wherein $S_{650-720EcoRI}$ designates the nucleotide sequence SEQ ID NO: 9, a nucleotide sequence complementary thereto, or a nucleotide sequence with a sequence identity of at least 95% thereto;

25 wherein P_2 designates the nucleotide sequence SEQ ID NO: 43, a nucleotide sequence complementary thereto, or a nucleotide sequence with a sequence identity of at least 85% thereto;

wherein $S_{1265gp120}$ designates the nucleotide sequence SEQ ID NO: 19, a nucleotide sequence complementary thereto, or a nucleotide sequence with a sequence identity of at least 70% thereto;

wherein $S_{1265XhoI}$ designates the nucleotide sequence SEQ ID NO: 17, a nucleotide sequence complementary thereto, or a nucleotide sequence with a sequence identity of at least 80% thereto;

wherein $S_{1465PstII}$ designates the nucleotide sequence SEQ ID NO: 23, a nucleotide sequence complementary thereto, or a nucleotide sequence with a sequence identity of at least 90% thereto;

wherein P_{4gp140} designates the nucleotide sequence SEQ ID NO: 57, a nucleotide sequence complementary thereto, or a nucleotide sequence with a sequence identity of at least 85% thereto;

wherein P_{4gp150} designates the nucleotide sequence SEQ ID NO: 55, a nucleotide sequence
5 complementary thereto, or a nucleotide sequence with a sequence identity of at least 85% thereto;

wherein P_{4gp160} designates the nucleotide sequence SEQ ID NO: 53, a nucleotide sequence complementary thereto, or a nucleotide sequence with a sequence identity of at least 85% thereto;

10 wherein S_{2060SacII} designates the nucleotide sequence SEQ ID NO: 33, a nucleotide sequence complementary thereto, or a nucleotide sequence with a sequence identity of at least 98% thereto; and

wherein P₅ designates the nucleotide sequence SEQ ID NO: 59, a nucleotide sequence complementary thereto, or a nucleotide sequence with a sequence identity of at least 85%
15 thereto.

The design of the parent synthetic BX08 gp160 envelope cassette gene with its variant length genes gp150, gp140, gp120 is outlined in figure 2.

20 The nucleotide sequence construct with the formula (I)

(I) P₁-S_{495ClaI}-S_{650-720EcoRI}-P₂-S_{1265gp120}

(visualised in figure 3) (SEQ ID NO: 73) codes for the amino acid sequence of gp120 (SEQ ID NO: 74). This amino acid sequence is the part of the HIV envelope that is secreted. Thus, it contains the immunogenic epitopes without being bound to the cell membrane. This is of
25 particular advantage if the nucleotide sequence construct is used for production of recombinant antigens or for a DNA vaccine as the antibody immune response may be higher to secreted versus membrane bound HIV antigens.

The nucleotide sequence construct with the formula (II)

30 (II) P₁-S_{495ClaI}-S_{650-720EcoRI}-P₂-S_{1265XhoI}-S_{1465PstI}-P_{4gp140}

(visualised in figure 4) (SEQ ID NO: 67) codes for the amino acid sequence of gp140 (SEQ ID NO: 68). This amino acid sequence encodes the gp120 and the extracellular part of the gp41 protein. The amino acid sequence is secreted due to the lack of the transmembrane spanning region. This is of particular advantage if the nucleotide sequence construct is used
35 for production of recombinant antigens as the immunogenic and/or antigenic epitopes in the extracellular part of gp41 are included and is of particular advantage for a DNA vaccine as

the antibody immune response may be higher to secreted gp120 versus membrane bound HIV antigens.

The nucleotide sequence construct with the formula (III)

5 (III) $P_1-S_{495}Clal-S_{650-720}EcoRI-P_2-S_{1265}XhoI-S_{1465}PstI-P_{4gp150}$

(visualised in figure 5) (SEQ ID NO: 69) codes for the amino acid sequence of gp150 (SEQ ID NO: 70). This amino acid sequence contains all of the envelope protein gp160 except the c-terminal tyrosin containing internalisation signals in the intracellular part of gp41. The membrane bound surface expression of the amino acid sequence is thereby maintained and
10 enhanced. Mimicking the organisation of the native epitope conformation may be expected, making this nucleotide sequence construct of particular advantage if the nucleotide sequence construct is used as a vaccine.

The nucleotide sequence construct with the formula (IV)

15 (IV) $P_1-S_{495}Clal-S_{650-720}EcoRI-P_2-S_{1265}XhoI-S_{1465}PstI-P_{4gp160}-S_{2060}SacII-P_5$

(visualised in figure 6) (SEQ ID NO: 71) codes for the amino acid sequence of gp160 (SEQ ID NO: 72) i.e. the entire envelope.

The nucleotide sequence construct designated P_1 comprises the nucleotide sequence

20 encoding the amino acid sequence in the first variable region (V1) and the amino acid sequence in the second variable region (V2). In one embodiment of the invention the first variable region is surrounded by EcoRV and PstI restriction enzyme sites, and the second variable region is surrounded by PstI and Clal restriction enzyme sites but as stated above, the choice of restriction enzyme sites can alter.

25

The nucleotide sequence construct designated $S_{650-720}EcoRI$ comprises the nucleotide sequence encoding the amino acid sequence in the third variable region (V3). In one embodiment of the present invention $S_{650-720}EcoRI$ is characterised by the restriction enzyme sites EcoRI and XbaI in the terminals.

30

The nucleotide sequence construct designated P_2 comprises the nucleotide sequence encoding the amino acid sequence of the fourth variable and constant region (V4 and C4). In one embodiment of the present invention the forth variable region is surrounded by SacI and XhoI restriction enzyme sites.

35

The nucleotide sequence construct designated S_{1265gp120} comprises the nucleotide sequence encoding amino acid sequence of the fifth variable and constant region (V5 and C5).

S_{1265gp120} further comprises a nucleotide sequence encoding a C-terminal stop codon.

- 5 The nucleotide sequence construct designated P_{4gp140} comprises the nucleotide sequence encoding amino acid sequence of the transmembrane spanning region. P_{4gp140} further comprises a nucleotide sequence encoding a C-terminal stop codon prior to the transmembrane spanning region.
- 10 The nucleotide sequence construct designated P_{4gp160} comprises the nucleotide sequence encoding amino acid sequence of the transmembrane spanning region (trans membrane spanning domain: TMD). In a preferred embodiment of the present invention the transmembrane spanning region is surrounded by HindIII and SacII restriction enzyme sites.
- 15 The term "sequence identity" indicates the degree of identity between two amino acid sequences or between two nucleotide sequences calculated by the Wilbur-Lipman alignment method (Wilbur et al, 1983).

The nucleotide sequence constructs with the formula (I), (II), (III), or (IV) illustrates the

- 20 flexibility in the present invention. By producing a gene with the described method enables the production of a plethora of antigens with various immunogenic epitopes and various advantages for production and vaccine purposes. To further illustrate the flexibility of the invention, other changes and mutations are suggested below.
- 25 In order to improve the immunogenicity of the nucleotide sequence constructs of the invention it is suggested to change the nucleotide sequence such that one or more glycosylation sites are removed in the amino acid sequence. By removal of shielding glycosylations, epitopes are revealed to the immunesystem of the mammal rendering the construct more immunogenic. The increased immunogenicity can be determined by an
- 30 improved virus neutralisation. Changes in the nucleotide sequence such that one or more N-linked glycosylation sites are removed in the amino acid sequence is well known by the person skilled in the art. Potential glycosylation sites are N in the amino acid sequences N-X-T or N-X-S (wherein X is any amino acid besides P). The glycosylation site can be removed by changing N to any amino acid, changing X to a P, or changing T to any amino acid. It is
- 35 preferred that N is changed to Q by an A to C mutation at the first nucleotide in the codon, and a C to G mutation at the third nucleotide in the codon. This is preferred to increase the

GC content in the nucleotide sequence construct. As an alternative N is changed to Q by an A to C mutation at the first nucleotide in the codon, and a C to A mutation at the third nucleotide in the codon. Preferred mutations in the synthetic BX08 envelope gene to remove potential N-linked glycosylation sites in V1 and/or V2 are A307C + C309A and/or A325C +
5 C327G and/or A340C + C342A and/or A385C + C387A and/or A469C + C471A. Examples of such changes is illustrated in SEQ ID NOs: 47, 49, and 51.

For historical reasons the HIVs have been divided into syncytia inducing strains and non syncytia inducing strains. The assay to determine whether a strain is syncytia inducing is
10 described in Verrier et al 1997, hereby incorporated by reference. It is presently known, that viruses utilising the CXCR4 co-receptor are syncytia inducing strains. It is also, at the present, known that the binding site for the CXCR4 involves the third variable region (V3). In a preferred embodiment the nucleotide sequence construct is changed to create a binding site for the CXCR4 co-receptor. It is presently performed in the third variable regions,
15 preferably by the mutation G865C + A866G.

It is well established that the HIV envelope comprises immunodominant epitopes. An immunodominant epitope is an epitope that most antibodies from the mammal are directed against. The antibodies directed against these immunodominant epitopes may have little
20 effect in elimination of the virus. It is therefore anticipated that modification of the immunodominant epitopes will induce antibodies directed against other parts of the envelope leading to a better elimination and neutralisation of the virus. By modification is understood any change in the nucleotide sequence encoding an immunodominant epitope in the amino acid sequence such that said amino acid sequence no longer contains an immunodominant
25 epitope. Thus, modification includes removal of the immunodominant epitope and decrease of immunogenicity performed by mutagenesis. In a preferred embodiment of the present invention an immunodominant epitope in the third variable region (V3) is modified, such as deleted or altered. In a much preferred embodiment the nucleotides 793-897 are deleted. In yet another preferred embodiment of the present invention an immunodominant epitope
30 has been removed from gp41, such as deleted. This is performed in P₇ or P₈ by elimination of the nucleotides 1654-1710.

It is anticipated that when gp120 is dissociated from gp41 in a vaccine or antigen, two immunodominant epitopes, one on each protein, are exposed and antibodies are directed
35 against these in the mammal. In the infectious virus, gp120 is coiled on top of gp41 and the gp120/gp41 is most likely organised in a trimer, so that these immunodominant epitopes are

hidden and therefore less elimination of virus is observed. By removing the cleavage site between gp41 and gp120 a full length gp160, gp150, or gp140 can be obtained with a covalent binding between gp41 and gp120. Removal of the cleavage site between gp41 and gp120 is preferably performed by a mutation at position C1423A. An example of such a
5 mutation is illustrated in the mutation of S₁₂₆₅XhoI (SEQ ID NO: 17) to S₁₂₆₅gp160 (SEQ ID NO: 21).

In order to stabilise the full length gp160, gp150, and gp140 for example when the cleavage site between gp41 and gp120 has been removed as described above, cysteins can be
10 inserted, preferably inside the gp41 helix creating disulphide bounds to stabilise a trimer of gp41s. In a preferred embodiment of the present invention the cysteins are inserted by the mutation 1618:CTCCAGGC:1625 to 1618:TGCTGCGG:1625. An example of such a change is illustrated in SEQ ID NO: 25.

15 The above mentioned decrease in immunodominant epitopes combined with the increase in immunogenicity of the other epitopes is expected to greatly enhance the efficacy of the nucleotide sequence construct as a vaccine.

During the production of the nucleotide sequence construct, it is convenient to ligate the
20 snuts into pieces. The pieces, as described above, are characterised by their reversible assembly as there are no duplicate restriction enzyme sites. In a preferred embodiment one piece (herein designated P₃) contains P₁, S₄₉₅ClaI, S₆₅₀₋₇₂₀EcoRI, and P₂. Another piece (herein designated P₈) contains S₁₂₆₅XhoI, S₁₄₆₅PstI, and P_{4gp160}. Yet another piece (herein designated P₇) contains S₁₂₆₅XhoI, S₁₄₆₅PstI, P_{4gp160}, S₂₀₈₀SacII, and P₅.

25 One advantage of the present nucleotide sequence construct is the easy access to exchange and alterations in the content and function of the nucleotide sequence and the encoded amino acid sequence. In one embodiment the nucleotide sequence coding for a functional region or parts thereof of the amino acid sequence is repeated. The repeat could
30 be back-to-back or a functional region or parts thereof could be repeated somewhere else in the sequence. Repeated could mean two (one repetition) but could also be three, six, or nine repeats. In a much preferred embodiment the repetition nucleotide sequence codes for amino acids in the third variable region.

35 In order to improve the protective capabilities of the invention against infections with HIV, one embodiment of the invention relates to the combination of epitopes. The present

nucleotide sequence construct allows insertion of one or more new nucleotide sequences isolated from another group and/or subtype of HIV and/or isolated from another patient. Hereby a vaccine or antigen with two or more epitopes from two or more HIVs is obtained. In a preferred embodiment, the V3 is replaced by the new nucleotide sequence. In a much
5 preferred embodiment, the new nucleotide sequence codes for amino acids in the third variable region of a different HIV isolate.

In order to improve the efficacy of the vaccine, aiming at raising cellular immunity, a nucleotide sequence coding for a T-helper cell epitope is included in the nucleotide
10 sequence construct. The nucleotide sequence coding for a T-helper cell epitope or a T-helper cell epitope containing amino acid sequence can be put in anywhere in the nucleotide sequence construct as long as it does not interact with the function of the envelope molecule. However, it is preferably placed in the tail of the nucleotide sequence construct or between the leader sequence and the envelope gene. The T-helper epitopes are preferably selected
15 from core proteins such as P24gag or from a non-HIV pathogen such as virus, bacteria, e.g. BCG antigen 85. For a therapeutic vaccine an HIV helper epitope is preferred since the patient is already primed by the HIV infection. For a prophylactic vaccine, a T-helper cell epitope from a frequently occurring non HIV pathogen such as Hepatitis B, BCG, CMV, EBV is preferred. Also, since the synthetic BX08 envelope genes may contain T-helper cell
20 epitopes in addition to important antibody epitopes, the synthetic BX08 vaccine genes can be mixed with other DNA vaccines to improve the efficacy of the other DNA vaccine.

One aspect of the present invention relates to individualised immunotherapy, wherein the virus from a newly diagnosed patient is directly cloned, the envelope or subunits
25 corresponding to snuts or pieces is produced with highly expressed codons, inserted into any of the nucleotide sequence constructs described above and administered to the patient as a vaccine. Hereby a therapeutic DNA vaccine is obtained, that will help the patient to break immunetolerance or induce/reinduce an appropriate immune response. In one embodiment the variable regions of the virus are produced with highly expressed codons and exchanged
30 into any of the nucleotide sequence constructs described above.

In one embodiment of the invention, the nucleotide sequence construct as described above satisfies at least one of the following criteria:

a) serum extracted from a Macaque primate which has been immunised by administration of
35 an expression vector containing the nucleotide sequence construct is capable of eliminating SHIV as determined by quantitative PCR and/or virus culturing.

b) serum extracted from a primate which has been immunised by administration of an expression vector containing the nucleotide sequence construct is capable of neutralising HIV-1 BX08 and /or other HIV-1 strains *in vitro*.

c) serum, extracted from a mouse which has been immunised by administration of an
5 expression vector containing the nucleotide sequence construct four times in intervals of three weeks and boosted after 15 weeks, is capable of decreasing the concentration of HIV-antigen in a culture of HIV, serum or PBMCs by at least 50%. An example of such procedure is shown in example 9.

10 In one embodiment of the invention, the nucleotide sequence construct of the invention, is used in medicine. That is, it is used as a vaccine, for the production of a recombinant protein, such that the recombinant protein is used as a vaccine, or the nucleotide sequence construct or the recombinant protein is used in a diagnostic composition.

Thus, the nucleotide sequence construct of the invention can be used for the manufacture of
15 a vaccine for the prophylactics of infection with HIV in humans.

Intramuscular inoculation of nucleotide constructs, i.e. DNA plasmids encoding proteins have been shown to result in the generation of the encoded protein *in situ* in muscle cells and dendritic cells. By using cDNA plasmids encoding viral proteins, both antibody and CTL
20 responses were generated, providing homologous and heterologous protection against subsequent challenge with either the homologous or cross-strain reaction, respectively. The standard techniques of molecular biology for preparing and purifying DNA constructs enable the preparation of the DNA therapeutics of this invention. While standard techniques of molecular biology are therefore sufficient for the production of the products of this
25 invention, the specific constructs disclosed herein provide novel therapeutics which can produce cross-strain protection, a result heretofore unattainable with standard inactivated whole virus or subunit protein vaccines.

The amount of expressible DNA to be introduced to a vaccine recipient will depend on the strength of the transcription and translation promoters used in the DNA construct, and on the
30 immunogenicity of the expressed gene product. In general, an immunologically or prophylactically effective dose of about 10 µg to 300 µg is administered directly into muscle tissue. Subcutaneous injection, intradermal introduction, impression through the skin, inoculation by gene gun preferably DNA coated gold particles, and other modes of administration such as intraperitoneal, intravenous, peroral, topic, vaginal, rectal, intranasal
35 or by inhalation delivery are also contemplated. It is also contemplated that booster

vaccinations are to be provided. It is further contemplated that booster vaccinations with recombinant antigens are to be provided, administered as described above.

The DNA may be naked, that is, unassociated with any proteins, adjuvants or other agents which impact on the recipients immune system. In this case, it is desirable for the DNA to be in a physiologically acceptable solution, such as, but not limited to, sterile saline or sterile buffered saline. Alternatively, the DNA may be associated with surfactants, liposomes, such as lecithin liposomes or other liposomes, such as ISCOMs, known in the art, as a DNA-liposome mixture, (see for example WO93/24640) or the DNA may be associated with and adjuvant known in the art to boost immune responses, such as a protein or other carrier. Agents which assist in the cellular uptake of DNA, such as, but not limited to, calcium ions, detergents, viral proteins and other transfection facilitating agents may also be used to advantage. These agents are generally referred to as transfection facilitating agents and as pharmaceutically acceptable carriers.

Those skilled in the field of molecular biology will understand that any of a wide variety of expression systems may be used. A wide range of suitable mammalian cells are available from a wide range of sources (e.g. the American Type Culture Collection, Rockland, Dm; also, see e.g. Ausubel et al. 1992). The method of transformation or transfection and the choice of expression vehicle will depend on the host system selected. Transformation and transfection methods are described e.g. in Ausubel et al 1992; expression vehicles may be chosen from those provided e.g. in P.H. Pouwels et al. 1985.

In one embodiment of the present invention the protein encoded by the nucleotide sequence construct is produced by introduction into a suitable mammalian cell to create a stably-transfected mammalian cell line capable of producing the recombinant protein. A number of vectors suitable for stable transfection of mammalian cells are available to the public e.g. in *Cloning Vectors: A Laboratory manual* (P.H. Pouwels et al. 1985); methods for constructing such cell lines are also publicly available, e.g. in Ausubel et al. 1992.

Standard reference works describing the general principles of recombinant DNA technology include Watson, J.D. et al 1987; Darnell, J.E. et al 1986; Old, R.W. et al, 1981; Maniatis, T. et al 1989; and Ausubel et al. 1992.

Figure legends

The invention is further illustrated in the following non-limiting examples and the drawing wherein

5 Figure 1 provides the codon preference of highly expressed proteins in human cells.

Figure 2 illustrates the outline of gp120, gp140, gp150, and gp160 encoding synthetic genes derived from the wild type sequence at the top. Variable (V) and constant (C) regions are shown together with the leader peptide (LP) and the transmembrane spanning domain (TMD). The approximate nucleotide positions of the restriction enzyme sites are shown. The approximate position of the three restriction enzyme sites dividing the full-length gp160 gene into the three pieces each containing only unique restriction enzyme sites are shown in bold.

15 Figure 3 building of the synthetic gp120 gene. Variable (V) and constant (C) regions are shown together with the leader peptide (LP) and the transmembrane spanning domain (TMD). The approximate nucleotide positions of the restriction enzyme sites are shown.

Figure 4 building of the synthetic gp140 gene. Variable (V) and constant (C) regions are shown together with the leader peptide (LP) and the transmembrane spanning domain (TMD). The approximate nucleotide positions of the restriction enzyme sites are shown.

Figure 5 building of the synthetic gp150 gene. Variable (V) and constant (C) regions are shown together with the leader peptide (LP) and the transmembrane spanning domain (TMD). The approximate nucleotide positions of the restriction enzyme sites are shown.

Figure 6 building of the synthetic gp160 gene. Variable (V) and constant (C) regions are shown together with the leader peptide (LP) and the transmembrane spanning domain (TMD). The approximate nucleotide positions of the restriction enzyme sites are shown

30

Figure 7 illustrates the codons coding amino acids in general

Figure 8 illustrates how overlapping PCR is performed.

35 Figure 9 illustrates how PCR using conserved flanking ends is performed.

Figure 10 illustrates how $S_{1265XhoI}$ is produced using complementary strands (minigene-approach) technology. The $S_{1265XhoI}$ is ligated from three sets of complementary strands into the vector pBluescript KS⁺ between restriction enzyme sites *XhoI* and *PstI*.

5

Figure 11 illustrates how $S_{1465PstI}$ is produced. The same approach, as the approach used for the production of $S_{1265XhoI}$, was used except that only two sets of complementary strands were used.

10 Figure 12 illustrates the assembly of P_1 . The $S_{O-N-Lang}$ and $S_{235EcoRV}$ are ligated into the *XbaI* and *PstI* site of the $S_{375PstI}$ containing plasmid.

Figure 13 illustrates the assembly of P_2 . The $S_{900XbaI}$ was excerted by *HindIII* and *SacI* from its plasmid and ligated with $S_{990SacI}$ (*SacI-SpeI*) into the $S_{110SpeI}$ plasmid that was opened

15 at the *HindIII* and *SpeI* sites.

Figure 14 illustrates the assembly of P_3 . $S_{495ClaI}$ (*ClaI-EcoRI*) and $S_{650-720EcoRI}$ (*EcoRI-XbaI*) and P_2 (*XbaI-XhoI*) were ligated simultaneously into the P_1 plasmid opened at the *ClaI* and *XhoI* sites to obtain the P_3 plasmid.

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Figure 15 illustrates the assembly of P_{4gp160} . $S_{1890HindIII}$ (*SacI-HindIII*) and $S_{1700EagI}$ (*HindIII-EagI*) were ligated simultaneously into the $S_{1630XbaI}$ plasmid opened by *SacI* and *EagI*.

Figure 16 illustrates the assembly of P_5 . $S_{2190ClaI}$ (*ClaI-PstI*) and $S_{2330PstI}$ (*PstI-EcoRI*) were
25 ligated into the S_{2425Es} plasmid opened by *ClaI* and *EcoRI*.

Figure 17 illustrates the assembly of P_{8gp160} . $S_{1465PstI}$ (*XbaI-PstI*) and $S_{1265XhoI}$ (*PstI-XhoI*) were ligated into the P_{4gp160} plasmid opened by *XbaI* and *XhoI*.

30 Figure 18 illustrates the assembly of P_{8gp150} . $S_{1465PstI}$ (*XbaI-PstI*) and $S_{1265XhoI}$ (*PstI-XhoI*) were ligated into the plasmid containing P_{4gp150} with the stop codon. P_{4gp150} plasmid was opened at the *XbaI* and *XhoI* sites for the ligation.

Figure 19 illustrates the assembly of P_{8gp140} . $S_{1465PstI}$ (*XbaI-PstI*) and $S_{1265XhoI}$ (*PstI-XhoI*) were
35 ligated into the plasmid containing P_{4gp140} with a stop codon. P_{4gp140} plasmid was opened at the *XbaI* and *XhoI* sites for the ligation.

Figure 20 illustrates the assembly of P_{8gp41} . Two complementary nucleotide strands 1265gp41S and 1265gp41AS designed with overhang creating a 5' *XhoI* and a 3' *PstI* restriction enzyme site were annealed and ligated into the piece 8 which is already opened at the *XhoI* and *PstI* sites whereby S_{1265} is deleted.

Figure 21 illustrates the assembly of P_7 . P_8 (*XhoI*-*SacII*) and $S_{2060SacII}$ (*SacII*-*Clal*) were ligated into P_5 plasmid opened at *XhoI* and *Clal*.

- 10 Figure 22a SDS PAGE of ^{35}S -labelled HIV-1 BX08 envelope glycoproteins radio-immuno precipitated from transiently transfected 293 cells using the indicated plasmids. Cell pellet (membrane bound antigens) or cell supernatant (secreted antigens) were precipitated by a polyclonal anti-HIV-1 antibody pool. Lane 1: untransfected cells. Lane 2: supernatant from syn.gp120_{MN} transfected cells. Lane 3: cell pellet from wt.gp160_{BX08} transfected cells.
- 15 Lane 4: cell pellet from cells co-transfected by wt.gp160_{BX08} and pRev. Lane 5: Mwt. marker. Lane 6: cell pellet from syn.gp160_{BX08} transfected 293 cells. Lane 7: cell pellet from syn.gp150_{BX08} transfected 293 cells. Lane 8: supernatant from syn.gp140_{BX08} transfected cells. Lane 9: supernatant from syn.gp120_{BX08} transfected cells.
- 20 Figure 22b is an SDS-PAGE of ^{35}S -labeled HIV-1 BX08 envelope glycoproteins radio-immune precipitated from transiently transfected 293 cells as cell pellet (membrane bound) or cell supernatant (secreted antigens) by anti-HIV-1 antibody pool using the indicated plasmids. Lane 1: untransfected 293 cells. Lane 2: cell pellet from syn.gp160MN transfected 293 cells as positive control (Vinner et al 1999). Lane 3: Cell supernatant from syn.gp120MN transfected 293 cells as positive control (Vinner et al 1999). Lane 4: Cell supernatant from syn.gp120BX08 transfected 293 cells demonstrating a glycoprotein band of 120 kDa. Lane 5: Cell supernatant from syn.gp140BX08 transfected 293 cells demonstrating a glycoprotein band of 120 kDa. Lane 6: Mwt. marker. Lane 7 at two different exposure times: Cell pellet from syn.gp150BX08 transfected 293 cells demonstrating a glycoprotein band of 120 kDa (lower gp30 band is not well seen in this exposure). Lane 8: Cell supernatant from syn.gp150BX08 transfected 293 cells showing no secreted proteins (all protein is membrane bound, see lane 7).
- 30

Figure 22c show fluorescent microscopy of U87.CD4.CCR5 cells transfected with BX08 gp160 genes plus pGFP. Panel A: cells transfected with empty WRG7079 vector plus pGFP showing no syncytia. Panel B: cells transfected with wild type BX08gp160 gene

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plus pGFP showing some syncytia. Panel C: cells transfected with synBX08gp160 plus pGFP showing extreme degree of syncytia formation. This demonstrates expression, functionality, and tropism of the expressed BX08 glycoprotein with much more expressed functionally active gp160 from the synthetic BX08 gene.

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Figure 23 shows the anti-Env-V3 BX08 antibody titers (IgG1). Panels show individual mice DNA immunized with syn.gp140BX08 plasmid either i.m. (left panel) or by gene gun (right panel), respectively. Immunization time points are indicated by arrows.

- 10 Figure 24 shows a Western Blotting of (from left to right) one control strip, followed by sere (1:50) from 2 mice i.m. immunized with synBX08gp120, 2 mice i.m. immunized with synBX08gp140, 2 mice i.m. immunized with synBX08gp150, and 2 mice immunized with synBX08gp160, followed by 2 mice gene gun immunized with synBX08gp120, 2 mice gene gun immunized with synBX08gp140, 2 mice gene gun immunized with synBX08gp150, and 2 mice gene gun immunized with synBX08gp160 respectively. Strip 5 is a mouse 5.1 DNA immunized i.m. with synBX08gp140 plasmid (same mouse as in figure 23). Plasma was examined at week 18. The positing of gp160 (spiked with four coupled gp51), gp120 and gp41 is indicated at the right. A positive reaction to HIV glycoproteins further demonstrates the mouse anti-HIV immunoglobulin reacting to HIV of a strain (IIIB) different from BX08 to illustrate cross-strain reactivity.
- 15
- 20

Figure 25 Theoretical example of calculation of the 50% inhibitory concentration (IC_{50}) values. IC_{50} for each mouse serum is determined by interpolation from the plots of percent inhibition versus the dilution of serum.

25

Figure 26 CTL responses were measured at week 18 to the mouse H-2D^d restricted BX08 V3 CTL epitope (IGPGGRAFYTT) for BALB/c mice (H-2D^d) i.m. immunized at week 0, 9, and 15 with the synthetic vaccine genes: syn.gp120_{BX08}, syn.gp140_{BX08}, syn.gp150_{BX08}, and syn.gp160_{BX08}, respectively, and median values of different E:T ratios for groups of mice are shown (26A). Intramuscular DNA immunization with syn.gp150_{BX08} induced a higher CTL response when injected i.m. in high amounts versus gene gun inoculation of skin (26B).

30

Figure 27 Summary of western immuno blotting assay of mice sera (1:40) collected at week 0, 9, and 18 from mice genetically immunized with syn.gp120_{BX08}, syn.gp140_{BX08},

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syn.gp150_{BX08}, syn.gp160_{BX08}, wt.gp160_{BX08}, and wt.gp160_{BX08} plus pRev, respectively. Percent responders in groups of 17-25 mice against gp120 and gp41 are shown.

Figure 28 IgG anti-rgp120 (IIIB) antibody titers of individual mice inoculated at week 0, 9, 15
5 (28A), or gene gun immunized at week 3, 6, 9, and 15 (28B) with the syn.gp150_{BX08} DNA vaccine.

Figure 29 IgG antibody titers to HIV-1 rgp120_{IIIB}. Median titers are shown from groups of
mice i.m. inoculated at week 0, 9, and 15 (29A), or gene gun immunized at week 0, 3, 6,
10 9, and 15 (29B) with the synthetic genes syn.gp120_{BX08}, syn.gp140_{BX08}, syn.gp150_{BX08},
and syn.gp160_{BX08}, respectively.

Examples

Example 1: Designing the nucleotide sequence construct

Initially the overall layout of the nucleotide sequence construct is decided. The overall layout comprises the various derivatives the gene will be expressed as. For BX08 these include, but
5 are not restricted to gp160, gp150, gp140, gp120, and gp41.

Next, the vehicle of expression (plasmid or virus) is to be determined: Preparation for a suitable vector determines both need for leader sequence, terminal restriction enzyme sites and whether or not an N- or C-terminal protein tag is to be considered (Poly-his, Myc-antibody-epitop, etc.). For BX08 a plasmid expression vehicle was chosen. All native wild
10 type HIV codons are systematically exchanged with the codons most frequently represented in a pool of highly expressed human genes (figure 1). By this exchange the amino acid sequence is conserved while the nucleotide sequence is dramatically altered. Thus, gene structures like overlapping reading frames (e.g. *vpu*, *rev*, and *tat*) or secondary structures (e.g. RRE) are most likely destroyed whereas protein cleavage sites, and glycosylation sites
15 are maintained. The 100% amino acid identity between wtBX08 and synthetic BX08 in the present examples should be calculated after the initial Ala-Ser amino acid sequence, as that sequence is a part of the 6 amino acid sequence long *NheI* restriction enzyme site.

Depending on the restriction enzyme sites located in the expression vector it is decided
20 which restriction enzyme sites can be present (tolerated) throughout the finished gene construct. The terminal restriction enzyme sites of the synthetic gene must remain unique to enable cloning into the vector chosen for expression. General requirements for restriction enzyme sites of choice: Preferably creating cohesive ends facilitating ligation, creating no compatible ends with adjacent restriction enzyme sites (e.g. *BamHI/BglII*), and being efficient
25 cutters. For BX08 the restriction enzyme sites accepted were the ones present in the polylinker of the pBluescript cloning vectors (*EagI*, *MluI*, *EcoRV*, *PstI*, *ClaI*, *EcoRI*, *XbaI*, *SacI*, *SpeI*, *XhoI*, *HindIII*, *SacII*, *NotI*, *BamHI*, *SmaI*, *Sall*, *DraI*, *KpnI* with the exception of *BglII* and *NheI*). This was decided to satisfy the original cloning strategy using individual cloning of snuts in pBluescript with restriction enzyme cleaved (trimmed) ends after PCR
30 amplification, which is not necessary when blunt-end cloning and assembling of complementary oligonucleotides are employed. All locations at which the selected restriction enzyme sites can be introduced by silent mutations (keeping 100% loyal to the amino acid sequence) are identified using the SILMUT software or equivalent.

From these possible restriction enzyme sites, a selection of restriction enzyme sites are introduced by silent nucleotide substitutions around functional regions of choice of the corresponding gene (e.g. RRE) or gene products (e.g. variable region 1 (V1), V2, V3, CD4 binding area, transmembrane domain, and regions of immunological significans, etc.).

- 5 Restriction enzyme sites are located at terminal positions of subcloned snuts (building entities) but additional restriction enzyme sites may be present within subunits. For BX08 the construct was initially to be cloned in the WRG7079 vector containing a tPA-leader sequence. Cloning sites were 5'-*NheI* → *BamHI*-3'. The entire humanised BX08 sequence was divided into thirds: 5'-*NheI* → *XhoI* → *SacII* → *BamHI*-3'. These sites were chosen in
- 10 this particular order because it resembles the polylinker of pBluescript (KS⁺) enabling successive ligations of the assembled thirds in this cloning vector. Within these thirds restriction enzyme sites were kept unique. Next, restriction enzyme sites were placed to flank the functional regions chosen as follows:
 - A. (5'-V1): *EcoRV*-235: Between C1 and V1. Alternatives: 3×*HindIII* (already excluded
 - 15 because exclusive use at position 1890) or *EcoRV*.
 - B. (V1-3'): Only alternative *PstI* 375.
 - C. (5'-V2): as B.
 - D. (V2-3'): Alternatives: *SpeI*, *Clal* 495. *Clal* chosen because it is closer to V2.
 - E. *EcoRI* 650 placed because next possible site was too far away.
 - 20 F. (5'-V3): *BglII* 720 was the alternative closest to the V3 region and further more unique.
 - G. (V3-3'): Alternatives *XhoI* (excluded) and *XbaI* 900 located very close to the V3 loop.
 - H. (5'-V4) *SacI* 990: alternatively *EcoRI* or *BamHI* (both excluded)
 - I. (V4-3'): Alternatives *SpeI* 1110, *KpnI* 1145, *PstI* 1135. *PstI* already used, *SpeI* chosen because of distance to previous site (*SacI* 990).
 - 25 J. (5'-V5): *XhoI* initially determined.
 - K. (Fusion peptide-3') *PstI* 1465 was the closest alternative to *XhoI* 1265.
 - L. (5'-Immunodominant region): *XbaI* 1630 chosen among *EcoRV* (blunt end), *PstI* and *XhoI* (both already used).
 - M. (Immunodominant region-3'): *EagI* 1700 perfect location.
 - 30 N. (C34 and C43 -3' (Chan, Fass, et al. 1997), and 5'-trans membrane domain): *SacII*. No alternatives.
 - O. (Trans membrane domain -3'): *SacII* 2060 already present.
 - P. *Clal* 2190 perfect position in relation to previous RE-site.
 - Q. *PstI* perfect position in relation to previous RE-site.
 - 35 R. *EcoRI* 2400 introduced to facilitate later substitution of terminal snut.
 - S. *BamHI* 2454 determined by the WRG7079 vector.

- Remove undesired restriction enzyme sites by nucleotide substitutions (keeping loyal to the amino acid sequence). Nucleotide substitution should preferably create codon frequently used in highly expressed human genes (figure 1). If that is not possible, the codons should
- 5 be the selected from the regular codons (figure 7). The substitutions made to the second nucleotide sequence to obtain desired restriction enzyme sites are shown in Table 2.

10 **Table 2 lists silent nucleotide substitutions in the humanised BX08 envelope sequence. Substitutions were made to create or delete restriction enzyme sites.**

Position:	substitution	Remarks:
138	c → g	creates Mlu I site on pos. 134-139
240	c → t	creates EcoRV site on pos. 238-243
501	c → a	creates Cla I site on pos. 501-506
502	a → t	do
503	g → c	do
504	c → g	do
657	c → a	creates EcoRI site on pos. 656-661
660	c → t	do
724	c → a	creates Bgl II site on pos. 724-729
726	c → g	do
727	a → t	do
728	g → c	do
729	c → t	do
840	c → t	EagI site is eliminated
904	a → t	creates Xba I site on pos. 904-909
905	g → c	do
906	c → t	do
907	c → a	do
909	c → a	do
994	a → t	creates Sac I site on pos. 990-995
995	g → c	do
1116	c → t	creates SpeI site on pos. 1114-1119
1119	c → t	do
1273	a → t	creates XhoI site on pos. 1272-1277
1274	g → c	do
1275	c → g	do
1293	c → t	Bgl II site is eliminated
1443	c → t	BstXI site is eliminated
1452	g → c	do
1467	c → t	PstI site on pos. 1466-1471
1470	c → a	do
1590	g → c	PstI site on pos. 1588-1593 is eliminated
1620	g → c	PstI site on pos. 1618-1623 is eliminated
1638	c → t	creates XbaI site on pos. 1638-1643
1641	g → a	do
1653	g → c	PstI site is eliminated
1687	a → t	PstI site is eliminated
1688	g → c	PstI site is eliminated
1710	c → g	creates EagI site on pos. 1709-1714
1758	c → t	Bgl II site is eliminated
1875	g → c	PstI site is eliminated
1893	c → a	Hind III on pos. 1893-1898
1897	c → t	do
1944	c → t	Bgl II site is eliminated

Position:	substitution	Remarks:
2199	c → t	Cla I site on pos. 2198-2203
2202	c → t	do
2203	c → t	do
2253	c → g	SacII site is eliminated
2292	g → c	PstI site is eliminated
2320	a → t	PstI site on pos. 2321-2326 is eliminated
2321	a → t	do
2322	g → t	do
2325	c → a	do
2430	c → a	creates EcoRI site on pos. 2429-2434
2433	c → t	do

Example 2: synthesis of oligos

In order to clone the individual snuts, nucleotide strands were synthesised or purchased. In total 28 synthetic nucleotide strands were synthesised. Nucleotide strands were synthesised

5 by standard 0.2 μ mol β -cyanoethyl-phosphoramidite chemistry on an Applied Biosystems DNA synthesiser model 392, employing 2000 Å CPG columns (Cruachem, Glasgow, Scotland), acetonitrile containing less than 0.001% water (Labscan, Dublin, Ireland) and standard DNA-synthesis chemicals from Cruachem, including phosphoramidites at 0.1 M and Tetrahydrofuran/N-methylimidazole as cap B solution. The nucleotide strands O-N-C

10 and 119MS-RC (for cloning of snut O-N-Lang), 650-E-BG and 720-XBAC-31 (for cloning of snut 650-720-EcoRI), 2425esup and 2425ESdo (for cloning of snut 2425-E-S) were synthesised with 5' end "trityl on" and purified on "Oligonucleotide Purification Cartridges" (Perkin Elmer, CA, USA) as described by the manufacturer. Other nucleotide strands (235-ECO5, 375-pst1.seq, 495-Cla1.seq, 900-XbaI, 990-sac1, 1110-SPE, 1630-Xba.seq, 1700-

15 Eag.seq, 17-Eag.seq, 1890-Hind.MPD, 2060-sac, 2190-cla, 2330-pst) were synthesised with 5' end "trityl off" and purified by standard ethanol precipitation. Oligoes 1265-1UP, 1265-1DO, 1265-2UP, 1265-2DO, 1265-3UP, 1265-3DO, 1465-1UP, 1465-1DO, 1465-2UP, 1465-2DO were purchased from Pharmacia.

Example 3: Cloning of snuts

- 20 The nucleotide sequence construct was designed in 17 DNA small pieces called snuts (Table 3) encompassing important structures like variable and constant regions each flanked with restriction enzyme (RE) sites to facilitate cassette exchange within each third of the gene: *NheI*-*XhoI*, *XhoI*-*SacII*, *SacII*-*BamHI*.
- 25 Each snut was cloned individually in a commercial vector (pBluescriptKS or pMOSblue) and kept as individual DNA plasmids, named after the snut which gives the nucleotide position of the RE in the BX08.

Table 3 list the snuts by their name and cloning vector.

Name	Cloning vector:
S _{O-N-Lang}	pMOSblue
S _{235EcoRV}	pMOSblue
S _{375PstI}	pBluescriptSK
S _{495ClaI}	pMOSblue
S _{650-720EcoRI}	pMOSblue
S _{900XbaI}	pMOSblue
S _{990SacI}	pMOSblue
S _{1110SpeI}	pMOSblue
S _{1265XhoI}	pBluescriptSK
S _{1465PstI}	pBluescriptSK
S _{1630XbaI}	pBluescriptSK
S _{1700EagI}	pBluescriptSK
S _{1890HindIII}	pBluescriptSK
S _{2060SacII}	pMOSblue
S _{2190ClaI}	pMOSblue
S _{2330PstI}	pMOSblue
S _{2425ES}	pBluescriptSK

Three principally different methods were used to obtain the dsDNA corresponding to each of
 5 the 17 snuts needed to build the synthetic BX08 genes.

1) "Overlapping" PCR: is based on the use of two ssDNA template nucleotide strands (forward and reverse) that complement each other in their 3'-end (figure 8). During the first PCR cycle, both templates annealed to each other at the 3'-ends allowing the full-length
 10 polymerisation of each complementary strand during the elongation step. The newly polymerized dsDNA strand are then amplified during the following cycles using an adequate forward and reverse primers set (figure 8).

Snut O-N-LANG: (S_{O-N-Lang}) two ng of the forward template nucleotide strands O-N-C and 2
 15 ng of the reward template-nucleotide strand 119MS-RC were mixed together with 50pmoles of the forward primer O-N-LANG-5 (5'-CTAGCTA-GCGCGCCGACCGCCT -3') and 50pmoles of the reverse primer O-N-LANG-3 (5'-CTCGATATCCTCGTGCATCTGCTC -3') in a 100µl PCR reaction volume containing 0.2mM dNTP's, 1x ExpandHF buffer with MgCl₂ (1.5mM) and 2.6 units of enzyme mix (Expand™ High fidelity PCR system from Boehringer
 20 Mannheim). The PCR was performed with the PE Amp 9600 thermocycler (Perkin Elmer) using the following cycle conditions: initial denaturation at 94°C for 30 sec., followed by 30 cycles of 94°C for 15 sec., 65°C for 30 sec., 72°C for 45 sec., with a final elongation at 72°C for 5 min., and cooling to 4°C.

Snut 650-720-EcoRI: ($S_{650-720EcoRI}$) PCR amplification was performed as described for snut O-N-LANG. One μ g of the forward ssDNA template-oligonucleotide 650-E-BG and 1 μ g of the reverse ssDNA template-oligonucleotide 720-XBAC were mixed with 40pmoles of the forward primer 650-E-5 (5'-CCGGAATT-CGCCCCGTGGTGAGCA-3') and 40 pmoles of the reverse primer 720-X-3 (5'-CTGCTCTAGAGATGTTGCAGTGGGCCT-3').

2) "Normal" PCR amplification: Eleven nucleotide strands: 235-ECO5, 375-pst1, 900-xba1, 990-sac1, 1110-SPE, 1630-XBA, 1700-EAG, 1890-HIN, 2060-sac, 2190-cla, and 2330-pst, were designed with common 5' and 3' flanking sequences which allowed PCR amplification with the same primer set (Forward primer : BX08-5 (5'-AGCGGATAACAATTTTCACACAGGA-3') and reverse primer : BX08-3 (5'-CGCCAGGGTTTTCCCAGTCACGAC-3') (Figure 9). The 495-Cla1 oligonucleotide was designed without a common flanking sequence and was therefore amplified with a specific set of primers 495-5N/495-3N (5'-GAATCGAT-CATCACCCAG-3' and 5'-GACGAATTCGTGGGTGCACT-3'). Each oligonucleotide was resuspended in 1ml of water and kept as a stock solution (approximately 0.2 mM). PCR amplification was performed with the Expand™ High Fidelity PCR System from Boehringer Mannheim (Cat. No. 1759078). Four concentrations of template nucleotide strand were systematically used: undiluted stock solution, stock solution 10^{-1} , stock solution 10^{-2} , stock solution 10^{-3} . One to 5 μ l of synthetic ssDNA template was amplified using the following conditions: BX08-5 (0.5 μ M), BX08-3 (0.5 μ M), 4 dNTP's (0.2mM), 1x ExpandHF buffer with $MgCl_2$ (1.5mM) and 2.6 units of enzyme mix. The PCR was performed using the PE Amp 9600 thermocycler (Perkin Elmer) using the following cycle conditions: initial denaturation at 94°C for 15 sec., followed by 30 cycles of 94°C for 15 sec., 65°C for 30 sec. and 72°C for 45 sec., with a final elongation at 72°C for 7 min., and cooling to 4°C.

25

3) *Minigene approach* : This method was used to synthesise $S_{1265XhoI}$, $S_{1465XbaI}$ and S_{2425ES} . **Snut 2425-E-S** (S_{2425ES}): 100 picomoles of each oligonucleotide 2425ES-up (35-mer ; 5'-AATTCGCCAGGGCTTCGAGCGCGCCCTGCTGTAAG-3') and 2425ES-do (35-mer ; GATCCTTACAGCAGGGCGCGCTCGAAGC-CCTGGCG-3') were mixed together in a 100 μ l final volume of annealing buffer containing NaCl 25mM, Tris 10mM and 1mM EDTA. After denaturation at 94°C for 15 min., the mixed oligonucleotides were allowed to anneal at 65°C during 15min.. The annealing temperature was allowed to slowly decrease from the 65°C to room temperature (22°C) during overnight incubation. The resulting double-strand dsDNA fragments harbored EcoRI- and BamHI-restriction sites overhangs that allowed direct cloning in pBluescript KS(+) vector using standard cloning techniques (Maniatis 1996).

35

Snut 1265-XhoI ($S_{1265XhoI}$): This snut was built according to the strategy depicted in figure 10. Three minigenes were constructed following the same method described for snut 2425-E-S. These minigenes are named 1265-1, 1265-2 and 1265-3. The minigene 1265-1 results from the annealing of the oligonucleotides 1265-1up (68-mer ; 5'-TCG AGC AGC GGC AAG GAG ATT
 5 TTC CGC CCC GGC GGC GGC GAC ATGC GCG ACA ACT GGC GCA GCG AGC T-3') and 1265-1do (68-mer ; 5'-GTA CAG CTC GCT GCG CCA GTT GTC GCG CAT GTC GCC GCC GCC GGG GCG G AAA ATC TCC TTG CCG CTG C-3'). 1265-2 results from the annealing of 1265-2up (61-mer ; 5'-GTA CAA GTA CAA GGT GGT GAA GAT CGA GCC CCT GGG CAT CGC CCC CAC CAA GGC CAA GCG C-3') and 1265-2do (63-mer ; 5'-CAC GCG GCG CTT GGC CTT GGT GGG GGC GAT GCC CAG GGG CTC GAT
 10 CTT CAC CAC CTT GTA CTT-3'). Finally, 1265-3 results from the annealing of 1265-3up (69-mer ; 5'-CGC GTG GTG CAG CGC GAG AAG CGC GCC GTG GGC ATC GGC GCT ATG TTC CTC GGC TTC CTG GGC GCT GCA-3') and 1265-3do (59-mer ; 5'-GCG CCC AGG AAG CCG AGG AAC ATA GCG CCG ATG CCC ACG GCG CGC TTC TCG CGC TGC AC-3'). Each minigene were designed in order to present single strand overhangs at their 5' and 3'- ends that allow easy ligation and XhoI-PstI
 15 direct cloning into pBlueScript KS+ vector.

Snut 1465-PstI ($S_{1465PstI}$): Two minigenes were constructed following the same methode described for snut 2425-E-S. These minigenes are named 1465-1 and 1465-2. The minigene 1465-1 was obtained after annealing of 1465-1up (90-mer : 5'-GGC AGC ACC ATG GGC GCC
 20 GCC AGC CTG ACC CTG ACC GTG CAG GCC CGC CAG CTG CTG AGC GGC ATC GTG CAG CAG CAG AAC AAC CTG CTG-3') and 1465-1do (98-mer : 5'-CGC GCA GCA GGT TGT TCT GCT GCT GCA CGA TGC CGC TCA GCA GCT GGC GGG CCT GCA CGG TCA GGG TCA GGC TGG CGG CGC CCA TGG TGC TGC CTG CA-3'), whereas minigene 1465-2 results from the annealing of 1465-2up (78-mer ; 5'-CGC GCC ATC GAG GCC CAG CAG CAC CTG CTC CAG CTGA CCG TGT GGG GCA TCA AGC AGC TCC
 25 AGG CCC GCG TGC TGG CT-3') and 1465-2do (78-mer ; 5'-CTA GAG CCA GCA CGC GGG CCT GGA GCT GCT TGA TGC CCC ACA CGG TCA GCT GGA GCA GGT GCT GCT GGG CCT CGA TGG-3'). Each minigene were designed in order to present single strand overhangs at their 5' and 3'- ends that allow easy ligation and PstI-XbaI direct cloning into pBlueScript KS+ vector using standard cloning techniques (Maniatis) (see figure 11).

30 **Example 4: assembly of snuts to pieces.**

The snut genes were then assembled into pieces (Table 4) so that unique restriction enzyme sites or mutagenesis can be used within each of these. This strategy will require fewer assemblings for optimal use of the cassette system. The following piece clones were made and kept individually for construction of the synBX08 gp160 gene (Figure 6):

Table 4 lists pieces by their name and their snut composition.

Piece name	snut composition	vector
P ₁	S _{O-N-LANG} -S _{235EcoRV} -S _{375PstI}	pBluescriptSK
P ₂	S _{900XbaI} -S _{990SacI} -S _{1110SpeI}	pMOSblue
P ₃	P ₁ -S _{495ClaI} -S ₆₅₀ -720EcoRI-P ₂	pBluescriptSK
P _{4gp160}	S _{1630XbaI} -S _{1700EagI} -S _{1890HinIII}	pBluescriptSK
P ₅	S _{2190ClaI} -S _{2330PstI} -S _{2425ES}	pBluescriptKS
P ₇	P _{8gp160} -S _{2060SacI} -P ₅	pBluescriptKS
P _{8gp160}	S _{1265XhoI} -S _{1465PstI} -P _{4gp160}	pBluescriptKS

Piece 1: The building strategy is shown in figure 12.

Preparation of the insert DNA: Five to 15µg of each plasmid O-N-LANG-cl7 and 235-EcoRV-cl5N, respectively, were double-digested by XbaI/EcoRV, and PstI/EcoRV, according to classical RE digestion procedure (Maniatis). The RE digestion products, were agarose gel purified according classical method (Maniatis). All RE digests were loaded on a 3% Nusieve 3:1(FMC), TBE 0.5X agarose gel and submitted to electrophoresis (7 Volts/mm during 2-3hours) until optimal fragment separation. The agarose-band containing the DNA fragments that correspond to the snut's sequence sizes (243-bp for O-N-LANG and 143-bp for 235-EcoRV) were excised from the gel. The DNA was extracted from agarose by centrifugation 20min at 5000g using a spin-X column (Costar cat#8160). Preparation of the vector: The snut 375-Pst1 klon1 was used as plasmid vector. Five µg were digested with XbaI and PstI. Removal of the polylinker XbaI/PstI fragment was performed by classical agarose gel purification, using a 0.9% Seakem-GTG agarose, TBE 0.5X gel. The linearised plasmid DNA was extracted from the agarose by filtration through spin-X column. All purified DNA fragments were quantified by spectrophotometry. Ligation: All three DNA fragments O-N-LANG (XbaI/EcoRV), 235-EcoRV (PstI/EcoRV) and 375-PstI(XbaI/PstI), were ligated together by classical ligation procedure, using an equimolar (vector:insert1:insert2) ratio of 1:1:1. Thus for, 200 ng (0.1 pmole) of XbaI/PstI-linearised 375-PstI-cl1 were mixed with 16 ng of O-N-LANG (XbaI/EcoRV) and 10 ng of 235-EcoRV (PstI/EcoRV) in a final reaction volume of 20µl of 1X ligation buffer containing 10U of T4 DNA ligase (Biolabs, cat#202S). The ligation was allowed overnight at 16°C. Transformation: Competent XL1-Blue bacteria (Stratagene cat#200130, transformation efficiency > 5•10⁶ col/µg) were transformed by classical heat-chock procedure : 1/10th of the pre-chilled ligation reaction was mixed with 50µl of competent bacteria. The mixture was allowed to stand in ice during 30 min. Bacteria were heat-shocked at 42°C during 45 sec. and then left 2 min. on ice before being resuspended in 450 µl of SOC medium. Transformed bacteria were incubated 1 hour at 37°C under shaking (250rpm) and plated on LB-ampicillin agar plates. The recombinant clones

were allowed to grow 16 hours at 37°C. Colony screening: 10 to 50 recombinant colonies were screened by direct PCR screening according to the protocole described into the pMOSBlue blunt-ended cloning kit booklet (RPN 5110, Amersham). Each colony was picked and resuspended in 50µl of water. DNA was freed by a boiling procedure (100°C, 5 min). Ten µl of bacterial lysate were mixed to 1 µl of a 10mM solution of premixed 4 dNTP's , 1 µl of M13reverse primer (5pmoles/µl, 5'-CAGGAAACAGCTATGAC-3'), 1 µl of T7 primer (5pmoles/µl, 5'-TAATACGACTCACTATAGGG-3'), 5µl of 10x Expand HF buffer 2 (Boehringer Mannheim, cat#1759078), 0.5µl of Enzyme mix (Boehringer Mannheim, 5U/µl) in a final volume of 50µl. DNA amplification was performed with a thermo-cycler PE9600 (Perkin-Elmer) using the following cycling parameters: 94°C, 2min, 35 cycles(94°C, 30sec; 50°C, 15sec; 72°C,30sec); 72°C, 5min; 4°C hold. Five µl of the PCR products were analysed after electrophoresis on a 0.9% SeakemGTG , 0.5xTBE agarose gel. Nucleotide sequence confirmation: ds-DNA was purified from minicultures of the selected clones with the JETstar mini plasmid purification system (Genomed Inc.). Sequencing was performed using

15 M13reverse and T7 primers and with the Big Dye™ Terminator Cycle Sequencing Ready reaction kit (Perkin-Elmer, Norwalk, Connecticut, P/N4303152) and the ABI-377 automated DNA sequenator (Applied Biosystems, Perkin-Elmer, Norwalk, Connecticut). Data were processed with the Sequence Navigator and Autoassembler softwares (Applied Biosystems, Perkin-Elmer, Norwalk, Connecticut).

20

Piece 2: The strategy for building that piece is depicted in figure 13. RE digestion, DNA fragments purification, ligation as well as direct PCR screening of recombinant colonies were performed according the same procedures described above for piece1, except the following:

- The linearised plasmid 1110-SpeI-cl24M1 was used as vector after being digested by
- 25 HindIII and SpeI, and agarose gel purified.
- A 166-bp HindIII/SacI, obtained from snut 900-XbaI-cl15, as well as a 130-bp SacI/SpeI fragment, obtained from snut 990-SacI-cl14, were agarose gel purified.
- Equimolar amount (0.1 pmoles) of the three DNA fragments described above were ligated in an one step ligation.
- 30 - 100µl of competent SCS110 bacteria (Stratagene cat# 200247) were transformed with 1/10th of the ligation products according to the manufactor instruction.
- Direct colony PCR screening was performed using T7 primer and pMOS-R (5'- GTTGTAACGACGGCCAG-3').

Piece 3: The strategy for building that piece is depicted in figure 14. RE digestion, DNA fragments purification, ligation as well as direct PCR screening of recombinant colonies were performed according the same procedures described above for piece1, except the following:

- The plasmid piece1-cl33 was linearised by ClaI and XhoI, in order to be used as vector,
5 and agarose gel purified.
- A 161-bp ClaI/EcoRI fragment, obtained from 495-ClaI-cl135M1 as well as a 254-bp EcoRI/XbaI fragment, obtained from 650-720-EcoRI-cl39, and a 374-bp XbaI/XhoI fragment, obtained from piece2-cl4, were agarose gel purified.
- Equimolar amount (0.1 pmole) of each of these 4 DNA fragments were mixed and ligated
10 together.
- 50µl of competent XL1Blue bacteria were transformed with 1/10th of the ligation products according to the protocole described for piece1.
- Direct colony PCR screening was performed using M13Reverse and T7 primers.

15 **Piece 4 gp160:** The strategy for building that piece is depicted in figure 15. RE digestion, DNA fragments purification, ligation as well as direct PCR screening of recombinant colonies were performed according the same procedures described above for piece1, except the following:

- The plasmid 1630-XbaI-cl2 was linearised by SacII/ EagI digestion and agarose gel
20 purified, in order to be used as vector.
- A 190-bp EagI/HindIII fragment, obtained from snut 1700-EagI-cl4, as well as a 177-bp SacII/HindIII fragment, obtained from snut 1890-HindIII-cl8, were agarose gel purified.
- Equimolar amount (0.1 pmoles) of the three DNA fragments described above were ligated in an one step ligation.
- 25 - 50µl of competent XL1Blue bacteria were transformed with 1/10th of the ligation products according to the protocole described for piece1.
- Direct colony PCR screening was performed using M13Reverse and T7 primers.

Piece 4-gp150: PCR-based site-directed mutagenesis was performed on double-stranded
30 plasmid-DNA from piece4-cl4 according an adaptation of the ExSite™ PCR-Based Site-Directed Mutagenesis Kit procedure (Stratagene cat#200502)(Weiner, M.P., Costa, G.L., Schoettlin, W., Cline, J., Marthur, E., and Bauer, J.C. (1994) Gene 151:119-123). The mutations introduced are shown in bold letters in the primer sequences below. PCR amplification was performed with the Expand™ High Fidelity PCR System (Boehringer
35 Mannheim, cat#1759078). Briefly, 1.5 µg, 0.5 µg or 0.1 µg of circular dsDNA was mixed with 1.5 pmoles of P4M2S (5'-TCTGGAAGCTCAGGGGGCTGCATCCCTGGC-3') and 1.5

pmoles of P4M2AS (5'-CCCGCCTGCCCCGTGTGACGGATCCAGCTCC-3') in a final volume of 50µl containing 4 dNTPs (250µM each), 1x Expand HF buffer 2 (Boehringer Mannheim, cat#1759078), 0.75µl of Enzyme mix (Boehringer Mannheim, 5U/µl). The PCR was performed with a PE9600 thermo-cycler (Perkin-Elmer Corporation) under the following cycling parameters : 94°C, 2min ; 15 cycles (94 °C, 45 sec ; 68 °C, 4 min); 72°C, 7min and 4 °C, hold. PCR products were phenol:chloroform extracted and precipitated (Maniatis). Plasmid template was removed from PCR products by DpnI treatment (Biolabs)(Nelson, M., and McClelland, M., 1992) followed by ethanol-precipitation. Amplicons were resuspended in 50 µl steril water, and phosphorylated according the following procedure: 7.5 µl of amplicons were mixed with 0.5µl of 100mM DTT, 1 µl of 10x pk buffer and 1 µl of pk mix enzyme (pMOSBlue blunt-ended cloning kit, Amersham , cat#RPN 5110). DNA kinasing was allowed 5min at 22°C. After heat-inactivation (10min, 75°C) of the pk enzyme, 1µl of ligase (4units, Amersham , cat#RPN 5110) was directly added to the pk reaction. The ligation was allowed overnight at 22°C. 50µl of competent XL1Blue bacteria were transformed with 1/10th of the ligation reaction according to the classical protocol (Maniatis). Insertion of mutations was checked by sequencing.

Piece 4-gp140: PCR-based site-directed mutagenesis was performed on piece 4-cl4, according to the procedure described for piece4-gp150 except that the primers P4M1AS (5'-TGTGTGACTGATTGAGGATCCCCAACTGGC-3') and P4S (5'-AGCTTGCCCACTTGTCAGCTGGAGCAGGT-3') were used.

Snut 1265-XhoI-gp120 : PCR-based site-directed mutagenesis was performed on plasmid 1265-XhoI-cl2M1 according to the procedure described for piece4-gp150 except that the primers 1265MAS (5'-CTTCTCGCGCTGCACCACGCGGCGCTTGGC-3') and 1265M2S (5'-CGCGCCTAGGGCATCGGCGCTATGTTCTC-3') were used.

Snut 1265-XhoI-gp160/uncleaved : PCR-based site-directed mutagenesis was performed on plasmid 1265-XhoI-cl2M1 according to the procedure described for piece4-gp150 except that the primers 1265MAS (5'-CTTCTCGCGCTGCACCACGCGGCGCTTGGC-3') and 1265M2S (5'-AGCGCCGTGGGCATCGGCGCTATGTTCTC-3') were used.

Snut 1465-PstI-CCG : PCR-based site-directed mutagenesis was performed on plasmid 1465-PstI-cl25 according to the procedure described for piece4-gp150 except that the primers 1465MAS (5'-CTGCTTGATGCCCCACACGGTCAGCTG-3') and 1465MS (5'-TGCTGCGGCCGCTGCTGGCTCTAGA-3') were used.

Piece 5 : The strategy for building that piece is depicted in figure 16. RE digestion, DNA fragments purification, ligation as well as direct PCR screening of recombinant colonies were performed according the same procedures described above for piece1, except the following:

- 5 - The plasmid 2425-ES-cl2 was linearised by ClaI/EcoRI digestion and agarose gel purified, in order to be used as vector.
- A 129-bp PstI/ClaI fragment, obtained 2190-ClaI-cl6M15, as well as a 114-bp PstI/EcoRI fragment, obtained from 2330-PstI-cl8, were agarose gel purified.
- Equimolar amount (0.1 pmoles) of the three DNA fragments described above were ligated
- 10 in an one step ligation.
- 50µl of competent XL1Blue bacteria were transformed with 1/10th of the ligation products according to the protocole described for piece1.
- Direct colony PCR screening was performed using T3 (5'-ATTAACCCTCACTAAAG-3') and T7 primers.

15

piece 8 : The strategy for building that piece is depicted in figure 17. RE digestion, DNA fragments purification, ligation as well as direct PCR screening of recombinant colonies were performed according the same procedures described above for piece1, except the following:

- The plasmid piece4-cl4 was linearised by XbaI/XhoI and agarose gel purified, in order to be
- 20 used as vector.
- A 200-bp XhoI/PstI fragment, obtained from 1265-XhoI-cl2M1 as well as a 178-bp PstI/XbaI fragment, obtained from 1465-PstI-cl25 were agarose gel purified.
- Equimolar amount (0.1 pmole) of these 3 DNA fragments were mixed and ligated together.
- 50µl of competent XL1Blue bacteria were transformed with 1/10th of the ligation products
- 25 according to the protocole described for piece1.
- Direct colony PCR screening was performed using T3 and T7 primers.

piece 8-gp150 : The strategy for building that piece was identical to that of piece 8, except that piece4-cl4M3 was used as vector (figure 18).

30

piece8-gp150/ uncleaved : The strategy for building that piece is identical to that of piece 8, except that piece4 gp160-cl4M3 is used as vector and a 200-bp XhoI/PstI fragment, obtained from snut 1265-XhoI-gp160/uncleaved as well as a 178-bp PstI/XbaI fragment, obtained from snut 1465-PstI-CCG are used like inserts.

35

piece 8-gp140 : The strategy for building that piece was identical to that of piece 8, except that piece4-cl4M5 was used as vector (figure19).

piece8-gp140/ uncleaved : The strategy for building that piece is identical to that of piece 8,
 5 except that piece4-cl4M5 is used as vector and a 200-bp XhoI/PstI fragment, obtained from snut 1265-XhoI-gp160/uncleaved as well as a 178-bp PstI/XbaI fragment, obtained from snut 1465-PstI-CCG are used like inserts.

Piece8-gp41 : The strategy for building that piece is depicted in figure 20. RE digestion,
 10 DNA fragments purification, ligation as well as direct PCR screening of recombinant colonies were performed according the same procedures described for synBX08 gp160 gene. A 63 bp linker is to be made according to the method described for snut 2425-ES, the minigene approach. Thus for 2 complementary oligonucleotides: 1265-gp41S(5'-
TCGAGgctagcGCCGTGGGCATCGGCGCTATGTTCTCGGCTTCCTGGGCGctgca-3') and
 15 1265-gp41AS (5'-gCGCCCAGGAAGCCGAGGAAC-
ATAGCGCCGATGCCACGGCgctagc-3') should be annealed together. This synthetic linker will be directly ligated into the XhoI /PstI sites of piece8-klon13 from which the snut 1265-XhoI-cl 2M1 would have been removed.

20 **piece7** : The strategy for building that piece is depicted in figure 21. RE digestion, DNA fragments purification, ligation as well as direct PCR screening of recombinant colonies were performed according the same procedures described above for piece1, except the following:

- The plasmid piece5-cl1 was linearised by ClaI/XhoI and agarose gel purified, in order to be used as vector,.
- 25 - A 798-bp XhoI/SacII fragment, obtained from piece8-cl13 as well as a 140-bp SacII/ClaI fragment, obtained from 2060-SacII-cl21 were agarose gel purified.
- The ligation of the 3 fragments was performed using a vector:insert ratio of 1:1, 1:2 or 1:5.
- 50µl of competent XL1Blue bacteria were transformed with 1/10th of the ligation products according to the protocole described for piece1.
- 30 - Direct colony PCR screening was performed using M13Reverse and T7 primers.

Example 5: assembly of genes

synBX08 gp160 gene : The strategy for building that gene is depicted in figure 6. RE digestion, DNA fragments purification, ligation as well as direct PCR screening of recombinant colonies were performed according the same procedures described for piece1
 35 20 µg of the expression plasmid WRG7079 were digested by NheI/BamHI. Plasmid DNA-

ends were dephosphorylated by Calf Intestin Phosphatase treatment (CIP, Biolabs) (Maniatis) to avoid autoligation of any partially digested vector. CIP enzyme was heat-inactivated and removed by classical phenol-chloroforme extraction. A 1277-bp NheI/XhoI fragment, obtained from piece3-cl27, as well as a 1194-bp XhoI/BamHI fragment, obtained from piece7-cl1, were agarose gel purified. The ligation was performed using a vector:insert ratio of 1:1 or 1:2. Fifty µl of competent XL1Blue bacteria were transformed with 1/10th of the ligation product according to the protocole described for piece1. After transformation bacteria were plated on LB-kanamycin agar plates. Direct PCR colony screening was performed using the primer set WRG-F (5'-AGACATAATAGCTGACAGAC-3') and WRG-R (5'-GATTGTATTTCTGTCCCTCAC-3'). The nucleotide sequence was determined according the methods described above for piece1.

synBX08 gp150 gene : The strategy for building that gene is depicted in figure 5. RE digestion, DNA fragments purification, ligation as well as direct PCR screening of recombinant colonies were performed according the same procedures described for synBX08 gp160 gene. A 1277-bp NheI/XhoI fragment, obtained from piece3-cl27, as well as a 800-bp XhoI/BamHI fragment, obtained from piece 8-gp150-cl26, were agarose gel purified and then ligated into the NheI/BamHI WRG7079 sites. The ligation was performed using a vector:insert ratio of 1:1 or 1:2.

For construction of the synthetic BX08 gp150, piece4 was mutated to Piece4gp150 whereby a tyrosine -> cysteine was changed and a stop codon was introduced after the transmembrane spanning domaine (TMD), followed by a BamHI cloning site. A new piece8gp150 was constructed composed of snut1265/snut1465/piece4gp150.

synBX08 gp150/uncleaved gene : RE digestion, DNA fragments purification, ligation as well as direct PCR screening of recombinant colonies are performed according the same procedures described for synBX08 gp160 gene. A 1277-bp NheI/XhoI fragment, obtained from piece3-cl27, as well as a 800-bp XhoI/BamHI fragment, obtained from piece 8-gp150/uncleaved, are agarose gel purified and then are ligated into the NheI/BamHI WRG7079 sites. The ligation was performed using a vector:insert ratio of 1:1 or 1:2.

synBX08 gp 140 gene : The strategy for building that gene is depicted in figure 4. RE digestion, DNA fragments purification, ligation as well as direct PCR screening of recombinant colonies were performed according the same procedures described for synBX08 gp160 gene. A 1277-bp NheI/XhoI fragment, obtained from piece3-cl27, as well as a 647-bp XhoI/BamHI fragment, obtained from piece 8-gp140-cl2, were agarose gel purified

and then ligated into the *NheI*/*Bam*HI sites of WRG7079. The ligation was performed using a vector:insert ratio of 1:1 or 1:2. For construction of the synthetic BX08 gp140, piece4 was mutated to Piece4gp140 whereby a stop codon was introduced just before the *TMD* followed by a *Bam*HI cloning site. A new piece8gp140 was constructed composed of

5 snut1265/1465/piece4gp140.

synBX08 gp140/uncleaved gene : RE digestion, DNA fragments purification, ligation as well as direct PCR screening of recombinant colonies are performed according the same procedures described for synBX08 gp160 gene. A 1277-bp *NheI*/*XhoI* fragment, obtained
10 from piece3-cl27, as well as a 800-bp *XhoI*/*Bam*HI fragment, obtained from piece 8-gp140/uncleaved, are agarose gel purified and then ligated into the *NheI*/*Bam*HI WRG7079 sites. The ligation was performed using a vector:insert ratio of 1:1 or 1:2.

synBX08 gp 120 gene : The strategy for building that piece is depicted in figure 3. RE
15 digestion, DNA fragments purification, ligation as well as direct PCR screening of recombinant colonies were performed according the same procedures described for synBX08 gp160 gene. A 1277-bp *NheI*/*XhoI* fragment, obtained from piece3-cl27, as well as a 206-bp *XhoI*/*Bam*HI fragment, obtained from 1265-*XhoI*-gp120-clM5, were agarose gel purified and then ligated into the *NheI*/*Bam*HI sites of WRG7079. The ligation was performed
20 using a vector:insert ratio of 1:1 or 1:2. For construction of the synthetic BX08 gp120, snut 1265 was mutated to S_{1265gp120} to introduce a stop codon at the gp120/gp41 cleavage site followed by a *Bam*HI cloning site.

The gp160, gp150, gp140, and gp120 genes are cloned (*NheI*-*Bam*HI) and maintained in an
25 eucaryotic expression vectors containing a CMV promotor and a tPA leader, but other expression vectors may be chosen based on other criteria e.g. antibiotic resistance selection, other leader sequences like CD5 etc, presence or not of immune stimulatory sequences etc.

SynBX08 gp41 gene : The strategy for building that gene is depicted in figure 20. RE
30 digestion, DNA fragments purification, ligation as well as direct PCR screening of recombinant colonies were performed according the same procedures described for synBX08 gp160 gene. Piece 8-gp41 is ligated with snut 2060-*Sac*II-klon21 and piece 5 as already decribed for the construction of piece 7, creating piece 7-gp41 (P_{7gp41}). Subsequently the piece 7-gp41 containing the entire gp41 gene will be cloned in WRG7079 using the *NheI*
35 and *Bam*HI sites.

Example 6a: High expression by codon optimization

To analyse the expression of glycoproteins from the wild type and synthetic BX08 envelope genes RIPA was performed on transfected mammalian cell lines. Both cell membrane associated and secreted HIV-1 glycoproteins from the cell supernatants were assayed. The
5 envelope plasmids were transfected into the human embryonic kidney cell line 293 (ATCC, Rockville, MD) or the mouse P815 (H-2D^d) cell line using calcium phosphate (CellPfect Transfection kit, Pharmacia). For radio immune precipitation assay (RIPA), transfected cells were incubated overnight, washed twice and incubated for 1 hour with DMEM lacking cysteine and methionine (Gibco). Then the medium was replaced with medium containing 50
10 μCi per ml of [³⁵S] cysteine and 50 $\mu\text{Ci}/\text{ml}$ of [³⁵S] methionine (Amersham Int., Amersham, UK) and incubation continued overnight. Cells were centrifuged, washed twice with HBSS and lysed in 1 ml ice-cold RIPA buffer (10 mM Tris, pH 7.4, 150 mM NaCl, 50 mM EDTA, 1% Nonidet P-40, 0.5% sodiumdeoxycholate) to detect *membrane bound* Env glycoproteins. The cell lysates were centrifuged for 15 min. at 100,000 $\times g$ to remove any undissolved particles
15 and 100 μl immune precipitated with protein A-sepharose coupled human polyclonal IgG anti-HIV antibodies (Nielsen et al., 1987). For analysis of secreted Env glycoproteins 500 μl of the 5 ml supernatants from transfected cells were incubated with protein A-sepharose coupled human polyclonal IgG anti-HIV antibodies. After washing three times in cold RIPA buffer and once in PBS, the immuno precipitates were boiled for 4 min. in 0.05 M Tris-HCl,
20 pH 6.8, 2% SDS, 10% 2-mercaptoethanol, 10% sucrose, 0.01% bromophenol blue and subjected to SDS PAGE (Vinner et al., 1999). Electrophoresis was carried out at 80 mV for 1 hour in the stacking gel containing 10% acrylamide, and at 30 mV for 18 hours in the separating gradient gel containing 5-15% acrylamide. Gels were fixed in 30% ethanol-10% acetic acid for 1 hour, soaked for 30 min. in En3Hance (Dupont #NEF 981), washed 2 \times 15
25 min. in distilled water, dried and autoradiography performed on Kodak XAR-5 film.

Transfection of human 293 cells with the syn.gp120_{BX08} and syn.gp140_{BX08} genes, respectively, resulted in high amounts of only secreted HIV-1 glycoproteins (Fig. 22a, lane 9 and 8). Thus, the synthetic gene in the absence of *rev* expresses the HIV-1 surface glycoprotein of the expected size which is recognised by human anti-HIV-1 antisera. The
30 expression of BX08 gp120 was Rev independent and with roughly the same high amount of gp120 from the syn.gp120MN gene (Fig. 22a, lane 2). Fig. 22a, lane 6 and lane 7 shows the expression of only membrane bound gp160 and gp150 from 293 cells transfected with syn.gp160_{BX08} and syn.gp150_{BX08} plasmids, respectively. Also transfection with wt.gp160_{BX08} plasmid resulted in a significant expression of membrane bound gp160 despite the absence
35 of Rev (Fig. 22a, lane 3). Co-transfection with equimolar amounts of Rev encoding plasmid seemed to increase this expression somewhat (Fig. 22a, lane 4). This is seen despite the

lower transfection effectivity using two plasmids and the use of only half the amount of wt.gp160_{BX08} DNA when combined with pRev. The amounts of secreted HIV-1 glycoproteins from gp120 and gp141 accumulating in the cell supernatants seemed higher than the amounts of cell associated glycoproteins at the time of harvesting of the cells. Interestingly, the amounts of gp160 produced from the "humanized" gene were about equal to the amounts produced by the wt.gp160_{BX08} + pRev genes, respectively (Fig. 22a, lane 4 and 6). The processing of gp160, gp150 and gp140 into gp120 plus a gp41, or fractions of gp41, produced from wild type or synthetic genes in the 293 cell-line did not function well under these experimental conditions. Same phenomenon was seen in RIPA from 293-CD4 cells and HeLa-CD4 cells infected by HIV-1_{MN} (Vinner et al., 1999). Because of the absence of CCR5 these cell-lines could, however, not be infected by HIV-1 strain BX08.

Example 6b: Radio immuno precipitation assay (RIPA) of synthetic BX08 transfected cells showing expression of glycoproteins from synthetic BX08 env plasmids

The synthetic envelope plasmid DNA were transfected into the human embryonic kidney cell line 293 (ATCC, Rockville, MD) using calcium phosphate (CellPfect Transfection kit, Pharmacia). For immune precipitation analysis, transfected 293 cells were treated and analysed according to the method described in example 6a.

To analyse expression from these genes, an SDS-PAGE of the ³⁵S-labelled HIV-1 envelopes, immune precipitated from the transfected cells is shown in figure 22b. Both cell-membrane associated and secreted HIV-1 envelope glycoproteins in the cell supernatants were assayed. Transfection of 293 cells with the synthetic BX08 gene encoding gp120 (syn.gp120BX08) in lane 4, and syn.gp140BX08 (lane 5) that did not contain *rev* encoding regions, resulted in abundant amounts of HIV-1 gp120. Thus, the expressions were *Rev* independent and expressed in roughly same high amounts as the syn.gp120MN and syn.gp160MN genes (lane 3 and 2, respectively) already showed by our group and others to be markedly increased in comparison with HIV MN wild type genes including *rev* (Vinner et al 1999).

Transfection with syn.gp150 plasmid (lanes 7 and 8) resulted in significant expression of membrane associated gp120 and low detectable amounts of truncated form of gp41 (cell pellet in lane 7) with no detectable HIV-1 glycoprotein in the cell supernatant lane 8. It is concluded that the synthetic BX08 genes express the envelope glycoproteins of expected size which are recognised by human anti-HIV-1 antiserum.

Exampel 6C FACS

To quantitate the surface expression of HIV glycoproteins from the wild type and synthetic BX08 envelope genes transfection experiments were done and cell surface expression
 5 examined by FACS (flow cytometer).

10 $10 \mu\text{g}$ of the BX08 envelope plasmid (wild type BX08gp160 or synBX08gp160) plus $10 \mu\text{g}$ of an irrelevant carrier plasmid pBluescript were used to transfect a 80-90% confluent layer of 293 cells in tissue culture wells (25 cm^2) using the CellPect kit (Pharmacia). After 48 hours
 15 cells were Versene treated, washed and incubated with a mouse monoclonal IgG antibodies to HIV gp120 (NEA-9301, NENTM, Life-Science Products Inc., Boston) for time 30 min. on wet ice followed by washing in PBS, 3% FCS and incubation with Phyto-Erytrin (PE) labelled rat anti-mouse IgG1 (Cat #346270, Becton Dickinson) according to the manufacture. After washing the cells were fixed in PBS, 1% paraformaldehyd, 3% FCS, and analysed on a
 20 FACS (FACScan, Becton-Dicknsson). Table 5 show in duplicate expression of BX08 gp160 from 11 % of the cells transfected with wild type BX08 (number 1 and 2) compared to the 48 % of cells expression BX08 glycoprotein when transfected with the synthetic gene (number 3 and 4). Thus, a several fold higher expression is obtained using the synthetic BX08 gene.

20 **Table 5** FACS analysis of 293 cells transfected with synBX08gp160 (No 1 and 2) and wt.gp16+BX08 (No3 and 4) and stained with monoclonal antibodies to surface expressed HIV glycoproteins. A higher expression was obtained with the synthetic gene (mean 48%) as compared to the wild type gene (mean 11 %).

	50 ul	45 ul	A	B	C	C - A	C - B
1	syn.gp160BX08 +	pBluescript SK+	2,57	2,85	36,91	34,34	34,06
2	syn.gp160BX08 +	pBluescript SK+	2,83	2,14	58,42	55,59	56,28
3	wt.gp160BX08 +	pBluescript SK+	1,95	1,52	7,51	5,56	5,99
4	wt.gp160BX08 +	pBluescript SK+	2,97	1,42	14,41	11,44	12,99

A: No primary antibody added (control for unspecific secondary Ab binding)

25 B: Neither Primary Ab nor Secondary Ab added (autoflourescence control)

C: Primary Ab and secondary Ab added.

Example 6D Analyses of the surface expression and biological functionality

To analyse the surface expression and biological functionality from the wild type and
 30 synthetic BX08 envelope genes transfection experiments were done and cell fusion microscopically studied using HIV envelope receptor expressing cells.

10 µg of the BX08 envelope plasmid (wt.BX08gp160 or syn.BX08gp160 or empty WRG7079 vector plasmid) plus 5 µg of a plasmid (pEGFP, Clontech) expressing green fluorescent protein (GFP) were transfected into 2×10^6 adherent U87.CD4.CCR5 cells (NIH AIDS Res. & Reference program, catalog #4035) stably expressing CD4 and CCR5, using the CellPfect
5 transfection kit (Pharmacia). After 48 hours the cells were examined by microscopy and photographed (Fig 22c).

Fig 22c panel A show the negative control (empty WRG7079 plus pGFP) giving no syncytia. Panel B show cells transfected with the wild type BX08 gp160 plasmid where cell-to-cell fusion (syncytia) is seen. Panel C show cells transfected with the same amounts of
10 synBX08gp160 plasmid and demonstrating a much higher degree of cell-cell fusion. In fact most or all of the cells in the culture plate were fused at this time. This experiment show surface expression of functional HIV gp160 with tropism to the CCR5 receptor, as well as a much higher expression and biological activity from the synthetic BX08 gene as compared to the wild type equivalent.

15

Example 7: Gene inoculation of mice for immunization

6-7 weeks old female BALB/c mice were purchased from Bomholdtgaard, Denmak. Microbiological status was conventional and the mice were maintained in groups of 4/5 per cage with food and water ad libitum and artificially lighted 12 hours per day. Acclimatization
20 period was 2 days. Mice were anaesthetized with 0.2 ml i.p. of rohypnol:stesolid (1:3, v/v) and DNA inoculated by either i.m. injection of 50 µl 2 mg/ml of plasmid DNA in each tibia anterior muscle at week 0, 9, and 15 and terminated week 18; or gene gun inoculated on shaved abdominal skin using plasmid coated gold particles (0.95 µm particles, 2 µg DNA/mg gold, 0.5 mg gold/shot, 50-71% coating efficiency) with the hand held Helios® gene gun
25 device (BioRad) employing compressed (400 psi) Helium as the particle motive force. Mice were gene gun vaccinated at week 0, 3, 6, 9, 15, and terminated week 18.

Example 8: Serological assays

Western blotting. The induction of a humoral response to gp120 and gp41 antigens by *in*
30 *vivo* expression of the encoded glycoproteins from the synthetic BX08 genes was examined by western immuno blotting (Figure 27). Mouse antisera (1:40) were evaluated in western blotting using the commercial HIV BLOT 2.2 strips (Genelabs Diagnostic). The conjugate was a 1:200 dilution of the alkaline phosphatase-conjugated rabbit anti-mouse IgG (Dakopatts, Glostrup, Denmark). Buffers, incubation condition and colour development were

- used according to the manufacturer. In these western blotting strips the gp160 band from HIV-1 IIIB contain of an oligomeric form of gp41 in a higher concentration than the monomeric gp41 band on the strip (Genelabs Diagnostic). HIV-1_{IIIB} lysate is used in these commercial strips where the gp160 band is composed by addition of tetrameric gp41. All
- 5 preimmune sera tested negative in western blotting. Mice inoculated with syn.gp120_{BX08} showed antibody response to the heterologous gp120 of HIV-1 IIIB. Inclusion of the extracellular part of gp41 in the gene syn.gp140_{BX08} induced antibody reaction to both gp120 and gp41 in all mice. This confirms the *in vivo* expression of BX08 gp120 and the extracellular part of gp41. DNA vaccination with syn.gp160_{BX08} encoding the membrane
- 10 bound glycoprotein induced antibodies to gp120 and gp41 in 50% and 64% of the mice, respectively. DNA vaccination with syn.gp150_{BX08} induced detectable antibodies to gp120 and gp41 in 41% and 53%, respectively. Induction of different levels of antibodies could explain the difference in numbers of positive reactive mice sera in this qualitative western blotting.
- 15 **ELISA.** Mouse anti HIV-1 gp120 antibodies were measured by indirect ELISA. Briefly, wells of polystyrene plates Maxisorb (Nunc) were coated for 2 days at room temperature with HIV-1 IIIB recombinant gp120 (Intracel) at 0.2 µg/100 µl of carbonate buffer, pH 9.6. Before use the plates were blocked 1 hour at room temperature with 150 µl/well of washing buffer (PBS, 0.5 M NaCl, 1% Triton-X-100) plus 2% BSA and 2% skimmilk powder. After 3 x 1 min.
- 20 washings, mouse plasma was added at 100 µl/well diluted in blocking buffer and ELISA plates incubated for 90 min. at room temperature using a microtiter plate shaker. As standard curve we used a mouse monoclonal antibody to a conserved part of gp120 between V5-C5 (MRDNWRSELYKY) (#NEA-9301, NENTM Life Science Products, Inc., Boston, MA). As calibration control included on each plate we used a plasma pool from 10 mice vaccinated
- 25 with BX08 gp120. Plates were again washed 5 x 1 min. and incubated 1 hour at room temperature with 100 µl/well of HRP-conjugated rabbit anti-mouse IgG (#P260, Dakopatts, Glostrup, Denmark) diluted 1:1000 in blocking buffer. Colour was developed with 100 µl/well of peroxidase enzyme substrate consisting of 4 mg of o-phenylenediamine in 11 ml water plus 4 µl hydrogen peroxide (30%, w/w). The enzyme reaction was terminated after 30 min.
- 30 by 150 µl/well of 1M H₂SO₄. The optical density (OD) of wells was measured at 492 nm using a microplate photometer (Molecular Devices, Biotech-Line, Denmark). Anti-HIV-gp120 IgG titers were expressed as the reciprocal plasma dilution resulting in an OD_{492nm} value of 0.500. Mouse anti-HIV-1 BX08 antibodies were also measured by indirect peptide ELISAs as described above using a BX08 V3 peptide (SIHIGPGRAFYTGD) (Schafer, Copenhagen
- 35 Denmark).

The IgG antibody response to HIV-1_{IIIb} rgp120 quantitated by ELISA is seen in Fig. 28 and Fig. 29. No background activity was observed in preimmune sera or in sera from 4 mice immunized with empty WRG7079 vector in parallel with the BX08 genes. All mice inoculated with the synthetic BX08 genes either by gene gun or by i.m. injection responded and showed

5 a persistent and high titered (about 100-10,000) IgG response to rgp120 as exemplified in Fig. 4. When comparing the median titers for groups of mice (Fig. 29) a moderate antibody response was observed with the wt.gp160_{BX08}. Intramuscular and gene gun immunization with a mixture of wt.gp160_{BX08} plasmid plus Rev encoding plasmid did not increase this antibody response. This was found even when both plasmids were coated onto the same

10 gold particles to ensure co-transfection of single target cells. However, to ensure inoculation of equal amounts of total DNA only half of the amount of wt.BX08 plasmid was used when mixing with pRev which may have contributed to the lower antibody response when pRev was included. A 5-fold improvement of the antibody response was obtained using the syn.gp160_{BX08} gene. This antibody response seemed further improved using the

15 syn.gp150_{BX08} gene where the cytoplasmic internalization signals were eliminated but only using gene gun inoculation. For both the gene gun inoculation of skin and i.m injection the highest antibody titers to rgp120 were induced by genes encoding *secreted* gp120/gp140 glycoproteins versus *membrane bound* gp150/gp160 glycoproteins, respectively. In general, equal antibody and ELISA titers to rgp120 were obtained using gene gun and i.m. injection of

20 the BX08 vaccine genes.

Example 9: Neutralization assay

Mouse plasma was diluted in culture medium (RPMI-1640 medium (Gibco) supplemented with antibiotics (Gibco), Nystatin (Gibco) and 10% FCS (Bodinco)) and heat inactivated at 60°C for 30 min. Of the HIV-1 strain BX08 (50 TCID₅₀ per ml propagated in PBMC) 250 µl

25 was incubated for 1 hour at room temperature with 250 µl dilution of mouse serum (four five-fold dilutions of mouse serum, final dilutions 1:20 to 1:2500). After incubation 1×10^6 PBMC in 500 µl culture medium was added to the virus-serum mixture and incubated overnight at 37°C in 5% CO₂. Subsequently, eight replicates of 10^5 PBMC in 200 µl culture medium were cultured in 96-well culture plates (Nunc) at 37°C in 5% CO₂. After seven days in culture the

30 concentration of HIV antigen in the culture supernatant was quantitated using HIV antigen detection ELISA (Nielsen et al., 1987).

This ELISA is performed using human IgG, purified from high titered patient sera, both as capture antibody and biotin-linked as detecting antibody. In brief, anti-HIV-capture IgG diluted 1:4000 in PBS, 100 µl/well, are coated onto Immunoplates (Nunc) overnight at 4°C. After

35 washing five times in washing buffer 100 µl of supernatants are applied and incubated overnight

at 4°C. Plates are washed 5 times before incubation with 100 µl HIV-IgG conjugated with biotin diluted 1:1000 in dilution buffer, plus 10% HIV-1 sero-negative human plasma for 3 hours at room temperature. Five times 1 min. washing in washing buffer are followed by 30 min. incubation with 100 µl of 1:1000 avidine-peroxidase (Dako P347 diluted in dilution buffer). Six
5 times 1 min. washings, 5 in washing buffer and the last one are done in dH₂O before colour is developed with 100 µl of peroxidase enzyme substrate consisting of 4 mg of OPD in 11 ml water plus 4 µl hydrogen peroxide (30 %, w/w). The enzyme reaction is terminated after 30 minutes by additional 150 µl of 1M H₂SO₄.

The HIV antigen concentration in cultures, preincubated with mouse serum, was expressed
10 relatively to cultures without mouse serum (culture medium), and the percentage inhibitions of the different dilutions of mouse serum were calculated. The 50% inhibitory concentration (IC₅₀) for each mouse serum was determined by interpolation from the plots of percent inhibition versus the dilution of serum, and the neutralizing titer of the serum was expressed as the reciprocal value of the IC₅₀. In each set-up a human serum pool known to neutralise
15 other HIV-1 strains was included in the same dilutions as the mouse serum as a calibratin control. For assay of neutralization of the heterologous SHIV89.6P the MT-2-cell-killing format was used (Crawford et al., 1999). The assay stock of SHIV89.6P was grown in human PBMC.

The neutralizing IC₅₀ antibody titers of plasma pools from 10 mice from each group
20 were measured at different time points (week 0, 9, and 18). A positive background in some preimmune sera and thus in all week 0 serum pools was noted even after dilution and heat inactivation that was found earlier to lower this background. In general the neutralizing titers to BX08 virus of such serum pools were transient and low ranging from 1:6-1:150 above background (data not shown). A possible cross-neutralization reaction to a heterologous,
25 primary HIV-1 envelope was tested using the SHIV89.6P which is relevant in macaque models of AIDS and serum pools from mice DNA immunized i.m. with syn.gp140_{BX08}. Preimmune serum had a titer of 1:37, which is indicative of a slightly positive background, whereas the 18 week p.i. serum had a positive neutralizing titer of 1:254 above background.

30 **Example 10: CTL assay**

The cellular immune response in mice following gene gun or i.m. genetic immunization with the different vaccine plasmids were examined (Fig. 26). Spleen was removed aseptically and gently homogenised to single cell suspension, washed 3 times in RPMI-1640 supplemented with 10% FCS and resuspended to a final concentration of 5 x 10⁷ cell/ml. The cells were
35 then incubated 5 days with mitomycin-C treated (50 µg/ml for 1 hour) mouse P815 (H-2D^d)

stimulator cells at a ratio of 10:1 in medium supplemented with 5×10^{-5} M β -mercaptoethanol. For assay of CTL response to HIV-1 BX08, P815 stimulator cells and target cells were pulsed with 20 μ g/ml of the HIV-1 BX08 V3 peptide containing a conserved murine H-2D^d restricted CTL epitope (IGPGRAFYTT) (Lapham et al., 1996). After

5 stimulation, splenocytes were washed three times with RPMI-1640 supplemented with 10% FCS and resuspended to a final concentration of 5×10^6 cells/ml. 100 μ l of cell suspension was added in triplicate to U-bottom 96-well microtiter plates and a standard 4 hour ^{51}Cr -release assay performed (Marker et al., 1973).

All synthetic BX08 plasmids induced a high specific CTL response thus confirming the *in vivo* expression and *in vivo* immunogenicity. The highest CTL response was obtained with syn.gp150_{BX08} followed by syn.gp120_{BX08}-syn.gp140_{BX08}, and syn.gp160_{BX08}, respectively. Thus, the CTL response induced did not correlate with the antigen being secreted or not. However, i.m. DNA immunization with syn.gp150_{BX08} containing six putative CpG motifs induced a higher CTL response than gene gun immunization (Fig. 26). This difference could, 15 be explained by the high amount of DNA used in the i.m. injections.

The T-lymphocyte cytokine profile of spleen cells after ConA stimulation as well as serum antibody IgG_{2a}/IgG₁ at week 18 were investigated. Neither the IFN γ /IL-4 nor the IgG_{2a}/IgG₁ ratios, which both reflects a Th1-type of immune response, were significantly higher for the i.m. immunized mice when compared with gene gun immunized mice (student t-test and 20 Mann-Whitney U-test). Thus, the CTL response did not correlate with a certain Th-type of response and the DNA immunization technique did not bias the immune response using synthetic BX08 genes.

Example 11: Antibody responses to DNA vaccination with synBX08 env plasmid

25 A relatively low and variable antibody response (1 of 10 mice) was obtained with gene gun inoculation of the syn.gp140BX08 plasmid vaccine starting at week 9, figure 23, right panel. A higher numbers of responders 3/10 with high IgG1 antibody responses at an earlier onset (week 3-9) was obtained with the syn.gp140BX08 plasmid using i.m. injection, left panel. Sera from later time points may show more responders and/or higher titers but are not 30 assayed. However, these results show the induction of an antibody response to the BX08 V3 peptide by DNA vaccination using one of the described synthetic BX08 constructs.

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Claims

1. A method for producing a nucleotide sequence construct comprising the following steps:
 - a) obtaining a first nucleotide sequence of an HIV gene from a patient within the first 12
5 months of infection;
 - b) designing a second nucleotide sequence utilising the most frequent codons from mammalian highly expressed proteins to encode the same amino acid sequence as the first nucleotide sequence of a) encodes
 - c) redesigning the second nucleotide sequence of b) so that restriction enzyme sites
10 surrounds the regions of the nucleotide sequence which encode functional regions of the amino acid sequence and so that selected restriction enzyme sites are removed thereby obtaining a third nucleotide sequence encoding the same amino acid sequence as the first and the second nucleotide sequence of a) and b) encode;
 - d) redesigning the third nucleotide sequence of c) so that the terminal snuts contain
15 convenient restriction enzyme sites for cloning into an expression vehicle;
 - e) producing the snuts between restriction enzyme sites of c) and terminal snuts of d);
 - f) assembling the snut of step e) to form a nucleotide sequence construct.
2. A method according to claim 1, wherein the HIV gene is the gene encoding the envelope.
20
3. A method according to claim 1 or 2, wherein the HIV gene encodes one or more Gag proteins.
4. A method according to any of the preceding claims, wherein the HIV in step a) is in group
25 M, O or N
5. A method according to claim 4, wherein the HIV is a group M virus.
6. A method according to any of the preceding claims, wherein the HIV is subtype A, B, C, D,
30 E, F, G, H, I, or J.
7. A method according to claim 6, wherein the HIV is subtype B.
8. A method according to any of the preceding claims wherein the first nucleotide sequence
35 is obtained by direct cloning.

9. A method according to any of the preceding claims, wherein the HIV in step a) is isolated with the first 11 months of infection, such a 10, 9, 8, 7, 6, 5, 4, 3, 2, 1, or 0.5 month after infection.

5

10. A method according to any of the preceding claims, wherein the redesigning in step c) is carried out after the second nucleotide sequence of step b) has been divided into pieces, so that each piece comprises only different restriction enzyme sites.

10 11. A method according to claim 10, wherein the second nucleotide sequence of step b) is divided into 9 pieces, or 8, or 7, or 6, or 5, or 4, or 3, or 2 pieces.

12. A method according to claim 11, wherein the second nucleotide sequence of step b) is divided into 3 pieces.

15

13. A method according to any of the preceding claims, wherein the second nucleotide sequence of step b) is designed utilising the most frequent codons from human highly expressed proteins to encode the same amino acid sequence as the first nucleotide sequence of step a) encodes.

20

14. A nucleotide sequence construct obtainable by the method of any of claims 1-13.

15. A nucleotide sequence construct according to claim 14, wherein the nucleotide sequence encoding the amino acid sequence in the first variable region is surrounded by *EcoRV* and *PstI* restriction enzyme sites.

25

16. A nucleotide sequence construct according to claims 14 or 15, wherein the nucleotide sequence encoding the amino acid sequence in the second variable region is surrounded by *PstI* and *Clal* restriction enzyme sites.

30

17. A nucleotide sequence construct according to any of claims 14-16, wherein the nucleotide sequence encoding the amino acid sequence in the third variable region is surrounded by *Clal* and *EcoRI* restriction enzyme sites.

18. A nucleotide sequence construct according to any of claims 14-17, wherein the nucleotide sequence encoding the amino acid sequence in the transmembrane spanning region is surrounded by *HindIII* and *SacII* restriction enzyme sites.
- 5 19. A nucleotide sequence construct according to any of claims 14-18, wherein the nucleotide sequence encoding the amino acid sequence on both sites of the cleavage site is surrounded by *PstI* and *XbaI* restriction enzyme sites.
20. A nucleotide sequence construct in isolated form which has a nucleotide sequence with
 10 the general formula (I), (II), (III), or (IV) or subsequences thereof
- (I) $P_1-S_{495Clal}-S_{650-720EcoRI}-P_2-S_{1265gp120}$
- (II) $P_1-S_{495Clal}-S_{650-720EcoRI}-P_2-S_{1265XhoI}-S_{1465PstI}-P_{4gp140}$
- (III) $P_1-S_{495Clal}-S_{650-720EcoRI}-P_2-S_{1265XhoI}-S_{1465PstI}-P_{4gp150}$
- (IV) $P_1-S_{495Clal}-S_{650-720EcoRI}-P_2-S_{1265XhoI}-S_{1465PstI}-P_{4gp160}-S_{2060SacII}-P_5$
- 15 wherein P_1 designates the nucleotide sequence SEQ ID NO: 41, a nucleotide sequence complementary thereto, or a nucleotide sequence with a sequence identity of at least 90% thereto;
- wherein $S_{495Clal}$ designates the nucleotide sequence SEQ ID NO: 7, a nucleotide sequence complementary thereto, or a nucleotide sequence with a sequence identity of at least
 20 95% thereto;
- wherein $S_{650-720EcoRI}$ designates the nucleotide sequence SEQ ID NO: 9, a nucleotide sequence complementary thereto, or a nucleotide sequence with a sequence identity of at least 95% thereto;
- wherein P_2 designates the nucleotide sequence SEQ ID NO: 43, a nucleotide sequence
 25 complementary thereto, or a nucleotide sequence with a sequence identity of at least 85% thereto;
- wherein $S_{1265gp120}$ designates the nucleotide sequence SEQ ID NO: 19, a nucleotide sequence complementary thereto, or a nucleotide sequence with a sequence identity of at least 70% thereto;
- 30 wherein $S_{1265XhoI}$ designates the nucleotide sequence SEQ ID NO: 17, a nucleotide sequence complementary thereto, or a nucleotide sequence with a sequence identity of at least 80% thereto;
- wherein $S_{1465PstI}$ designates the nucleotide sequence SEQ ID NO: 23, a nucleotide sequence complementary thereto, or a nucleotide sequence with a sequence identity of at least 90%
 35 thereto;

wherein P_{4gp140} designates the nucleotide sequence SEQ ID NO: 57, a nucleotide sequence complementary thereto, or a nucleotide sequence with a sequence identity of at least 85% thereto;

wherein P_{4gp150} designates the nucleotide sequence SEQ ID NO: 55, a nucleotide sequence complementary thereto, or a nucleotide sequence with a sequence identity of at least 85% thereto;

wherein P_{4gp160} designates the nucleotide sequence SEQ ID NO: 53, a nucleotide sequence complementary thereto, or a nucleotide sequence with a sequence identity of at least 85% thereto;

wherein S_{2060SacII} designates the nucleotide sequence SEQ ID NO: 33, a nucleotide sequence complementary thereto, or a nucleotide sequence with a sequence identity of at least 98% thereto; and

wherein P₅ designates the nucleotide sequence SEQ ID NO: 59, a nucleotide sequence complementary thereto, or a nucleotide sequence with a sequence identity of at least 85% thereto.

21. A nucleotide sequence construct according to claim 20, with the formula (I)

(I) P₁-S_{495ClnI}-S_{650-720EcoRI}-P₂-S_{1265gp120}

22. A nucleotide sequence construct according to claim 20, with the formula (II)

(II) P₁-S_{495ClnI}-S_{650-720EcoRI}-P₂-S_{1265XhoI}-S_{1465PstI}-P_{4gp140}

23. A nucleotide sequence construct according to claim 20, with the formula (III)

(III) P₁-S_{495ClnI}-S_{650-720EcoRI}-P₂-S_{1265XhoI}-S_{1465PstI}-P_{4gp150}

24. A nucleotide sequence construct according to claim 20, with the formula (IV)

(IV) P₁-S_{495ClnI}-S_{650-720EcoRI}-P₂-S_{1265XhoI}-S_{1465PstI}-P_{4gp160}-S_{2060SacII}-P₅

25. A nucleotide sequence construct according to claim 20 consisting essentially of the subsequence P₁.

26. A nucleotide sequence construct according to claim 20 consisting essentially of the subsequence S_{495ClnI}.

27. A nucleotide sequence construct according to claim 20 consisting essentially of the subsequence S_{650-720EcoRI}.

28. A nucleotide sequence construct according to claim 20 consisting essentially of the subsequence P₂.
- 5 29. A nucleotide sequence construct according to claim 20 consisting essentially of the subsequence S_{1265gp120}.
30. A nucleotide sequence construct according to claim 20 consisting essentially of the subsequence S_{1265XhoI}.
- 10 31. A nucleotide sequence construct according to claim 20 consisting essentially of the subsequence S_{1465PstI}.
32. A nucleotide sequence construct according to claim 20 consisting essentially of the subsequence P_{4gp140}.
- 15 33. A nucleotide sequence construct according to claim 20 consisting essentially of the subsequence P_{4gp150}.
34. A nucleotide sequence construct according to claim 20 consisting essentially of the subsequence P_{4gp160}.
- 20 35. A nucleotide sequence construct according to claim 20 consisting essentially of the subsequence S_{2060SacII}.
- 25 36. A nucleotide sequence construct according to claim 20 consisting essentially of the subsequence P₅.
37. A nucleotide sequence construct with a sequence identity of more than 85% to the nucleotide sequence construct in any of claims 20-35.
- 30 38. A nucleotide sequence construct according to claim 37, wherein the sequence identity is more than 90% such as more than 95%, 98%, or 99%.
- 35 39. A nucleotide sequence construct according to claim 37, wherein the sequence identity is 100%.

40. A nucleotide sequence construct according to any of claims 14-39, coding for an HIV envelope or parts thereof with an improved immunogenicity obtained by mutating the nucleotide sequence construct of any of claims 14-39 such that one or more glycosylation
5 sites in the amino acid sequence have been removed.

41. A nucleotide sequence construct according to claim 40 with a mutation at positions A307C + C309A and/or A325C + C327G and/or A340C + C342A and/or A385C + C387A and/or A469C + C471A or any combination of those.
10

42. A nucleotide sequence construct according to any of claims 14-41, coding for an HIV envelope or parts thereof with a binding site for the CXCR4 co-receptor in the third variable region.

15 43. A nucleotide sequence construct according to claim 42 with a mutation at positions G865C + A866G.

44. A nucleotide sequence construct according to any of claims 14-43, coding for an HIV envelope or parts thereof, wherein an immunodominant epitope has been modified.
20

45. A nucleotide sequence construct according to claim 44, wherein an immunodominant epitope in the third variable region has been modified.

46. A nucleotide sequence construct according to claim 45 with a deletion of nucleotides
25 793-897.

47. A nucleotide sequence construct according to claim 44, wherein an immunodominant epitope has been removed from gp41.

30 48. A nucleotide sequence construct according to any of claims 14-47, coding for an HIV envelope or parts thereof, wherein the cleavage site between gp41 and gp120 is removed.

49. A nucleotide sequence construct according to claim 48 with a mutation at position
35 C1423A.

50. A nucleotide sequence construct according to claim 20 consisting essentially of the subsequence P₁, S₄₉₅ClaI, S₆₅₀₋₇₂₀EcoRI, and P₂.
51. A nucleotide sequence construct according to claim 20 consisting essentially of the
5 subsequence S₁₂₆₅XhoI, S₁₄₆₅PstI, and P_{4gp140}.
52. A nucleotide sequence construct according to claim 20 consisting essentially of the subsequence S₁₂₆₅XhoI, S₁₄₆₅PstI, P_{4gp160}, S₂₀₆₀SacII, and P₅.
- 10 53. A nucleotide sequence construct according to any of claims 14-52, further comprising a nucleotide sequence repeat coding for a functional region of the amino acid sequence.
54. A nucleotide sequence construct according to claim 53, wherein the nucleotide sequence repeat codes for amino acids in the third variable region.
- 15 55. A nucleotide sequence construct according to any of claim 14-54, further comprising a nucleotide sequence coding for a T-helper cell epitope containing sequence.
56. An expression vehicle selected from a group of viral vectors consisting of simliki forest
20 virus (sfv), adenovirus and Modified Vaccinia Virus Ankara (MVA), further comprising a nucleotide sequence construct according to any of claim 14-55.
57. A method of individualised immunotherapy wherein the virus from a newly diagnosed patient is directly cloned, the envelope is produced with highly expressed codons, inserted
25 into any of the nucleotide sequence constructs of claims 14-55, and administered to the patient.
58. Use of a nucleotide sequence construct according to any of claims 14-55 in medicine.
- 30 59. Use of a nucleotide sequence according to any of claims 14-55 for the manufacture of a vaccine for the prophylactics of infection with HIV in humans.
60. Use of a nucleotide sequence according to any of claims 14-55 for the manufacture of a
35 composition for the treatment of an HIV infection in a human within 24 weeks of primary infection.

61. Use of the nucleotide sequence according to any of claims 14-55 for the production of a recombinant protein.

1/33

Amino acid	One letter amino acid code	Three letter amino acid code	Codon
Alanine	A	Ala	GCC
Arginine	R	Arg	CGC
Asparagine	N	Asn	AAC
Aspartic acid	D	Asp	GAC
Cysteine	C	Cys	TGC
Glutamine	Q	Gln	CAG
Glutamic acid	E	Glu	GAG
Glycine	G	Gly	GGC
Histidine	H	His	CAC
Isoleucine	I	Ile	ATC
Leucine	L	Leu	CTG
Lysine	K	Lys	AAG
Proline	P	Pro	CCC
Phenylalanine	F	Phe	TTC
Serine	S	Ser	AGC
Threonine	T	Thr	ACC
Tyrosine	Y	Tyr	TAC
Valine	V	Val	GTG

Fig. 1

2/33

Synthetic BX08 Env Strategy for building the full-length gp160 and derived truncated forms

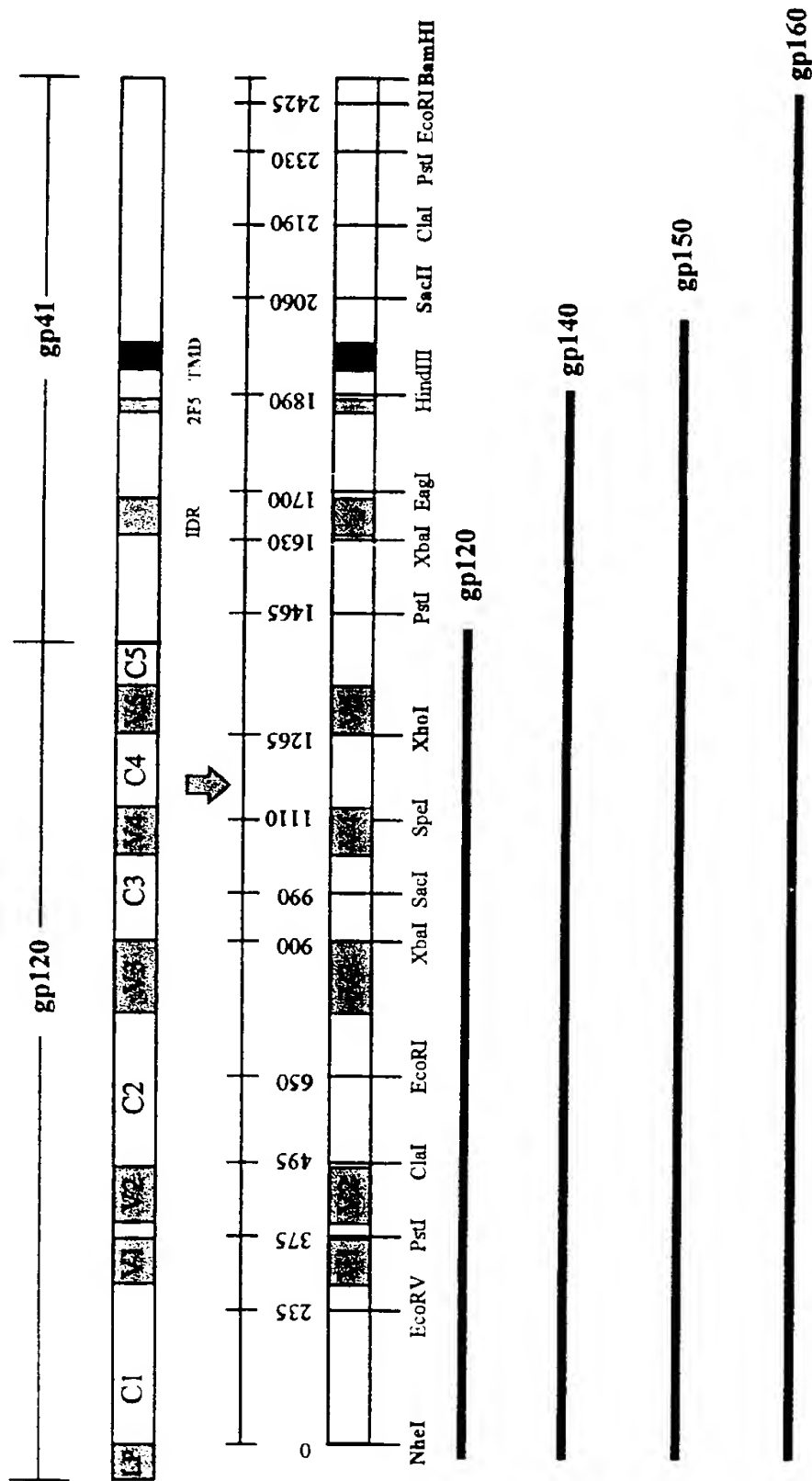


Fig. 2

3/33

Building of Synthetic BX08 Env (gp120)

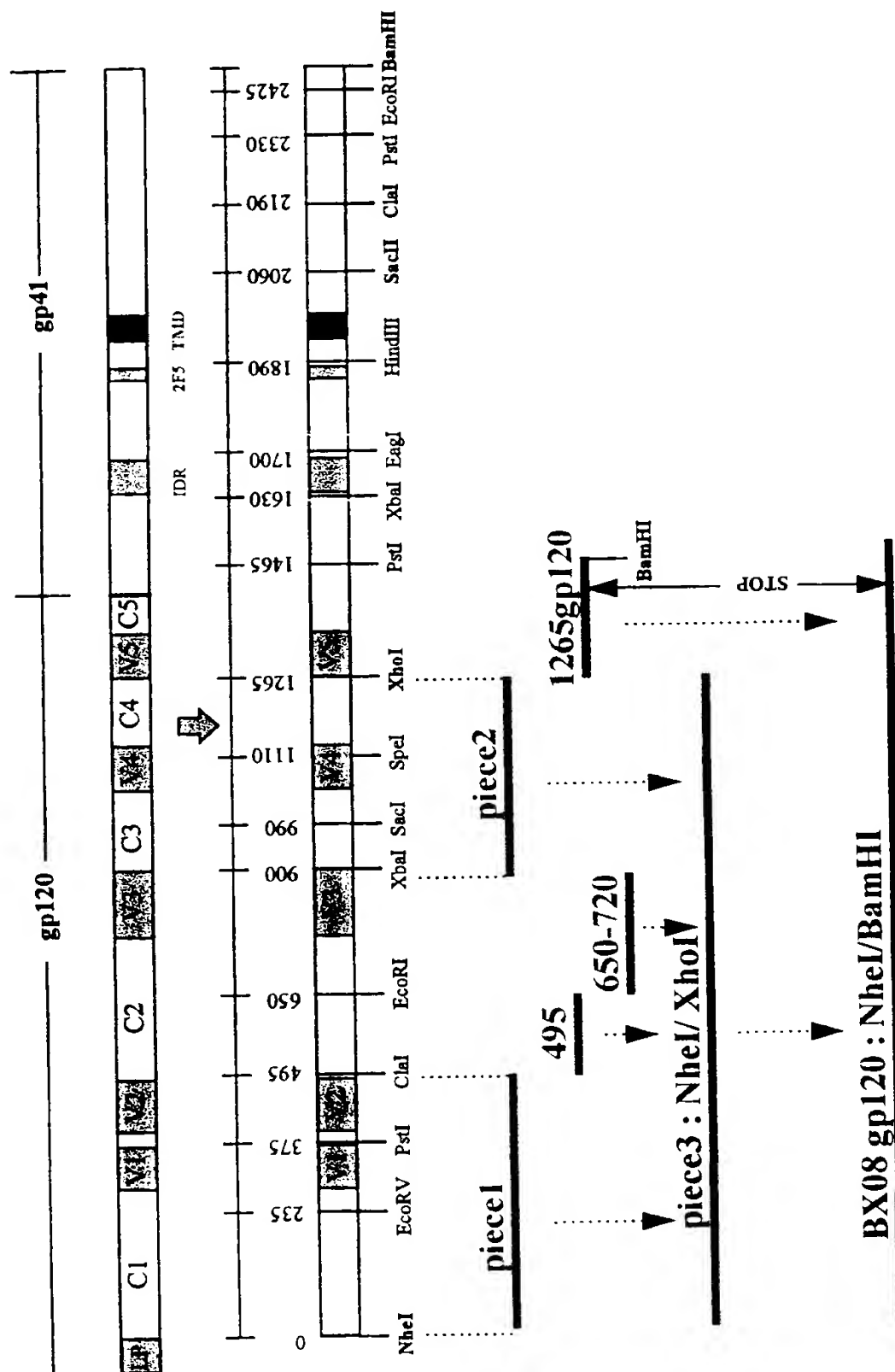


Fig. 3

4/33

Building of Synthetic BX08 Env (gp140)

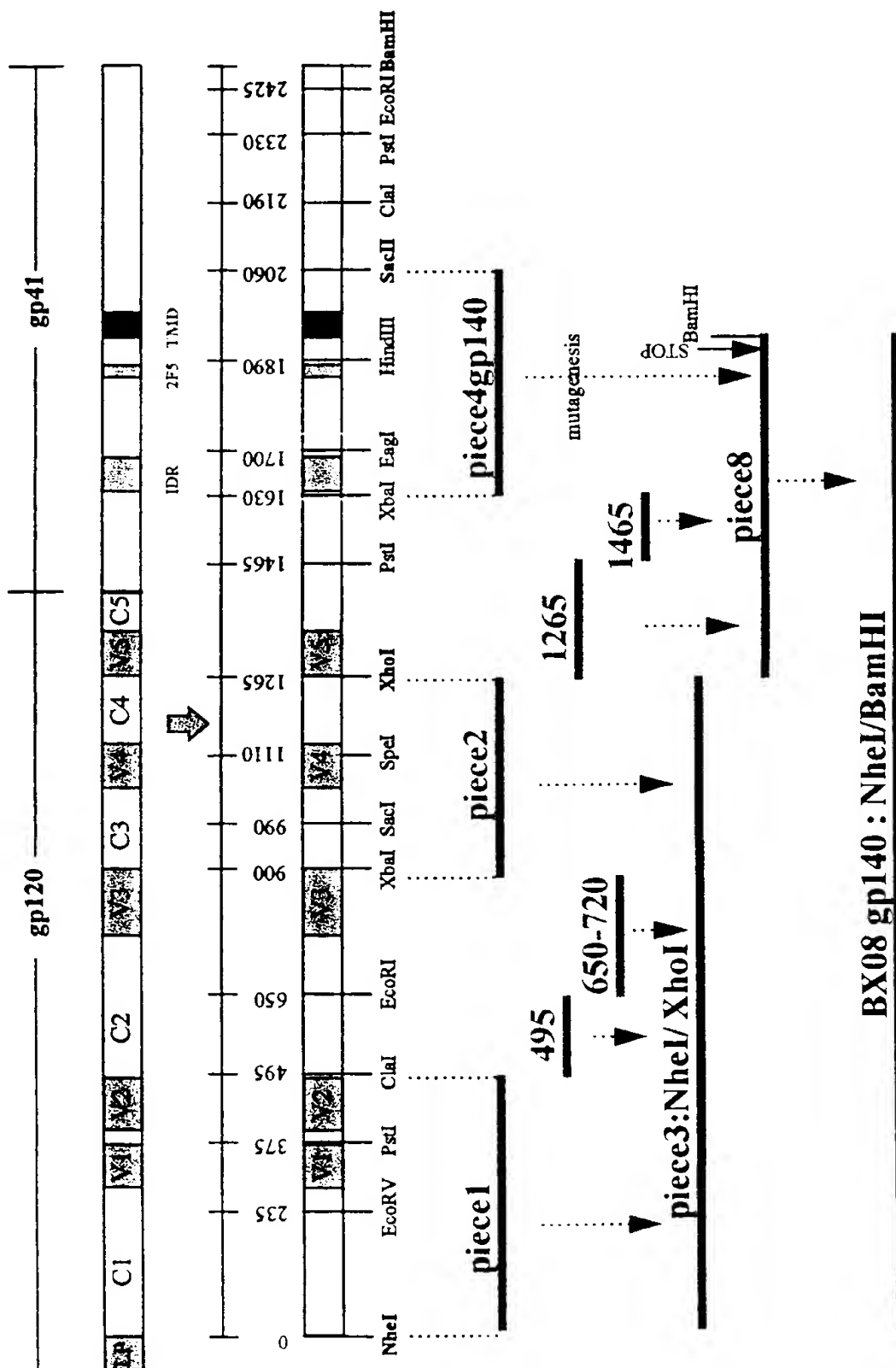


Fig. 4

Fig. 4

5/33

Building of Synthetic BX08 Env (gp150)

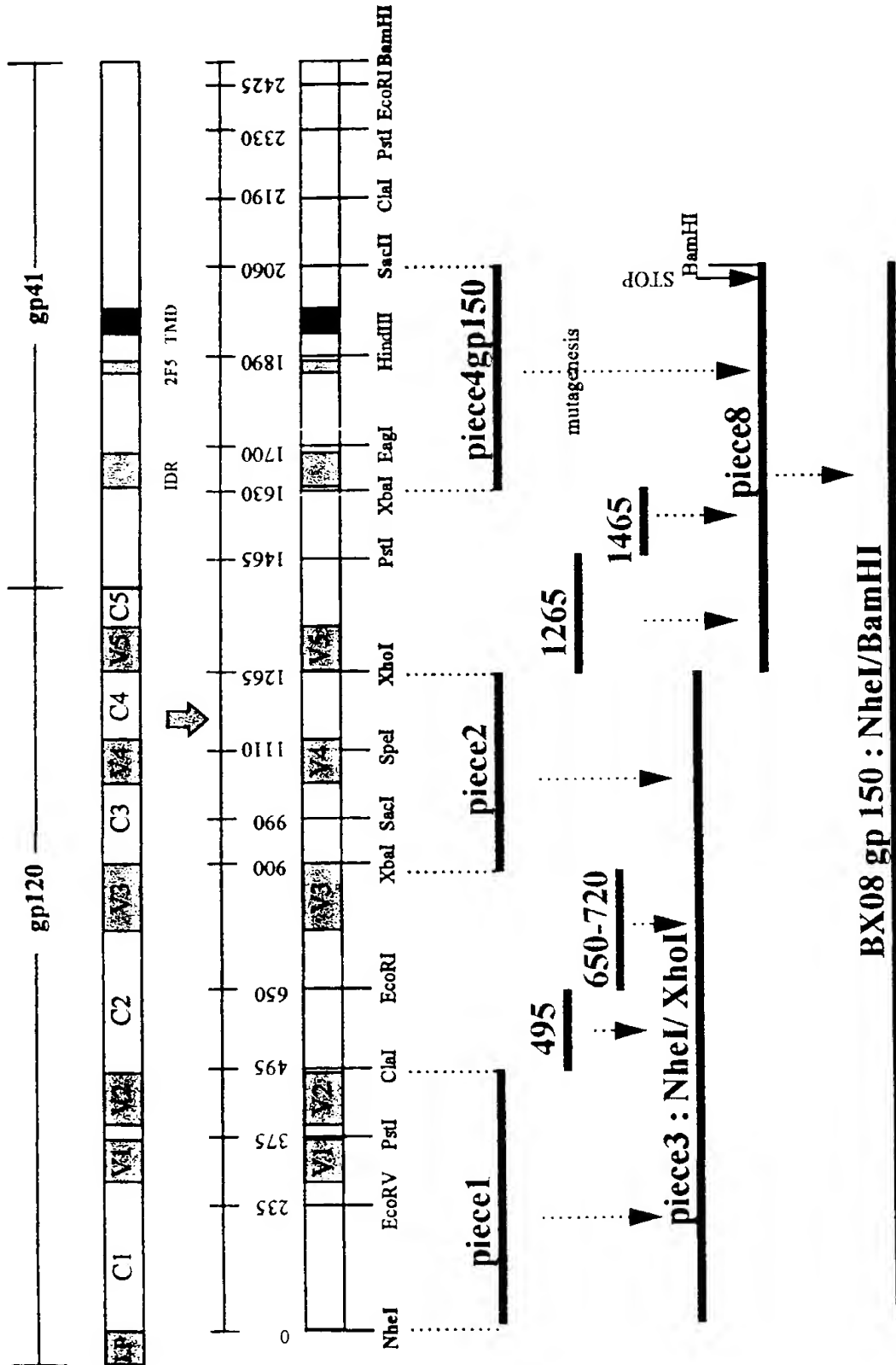


Fig. 5

6/33

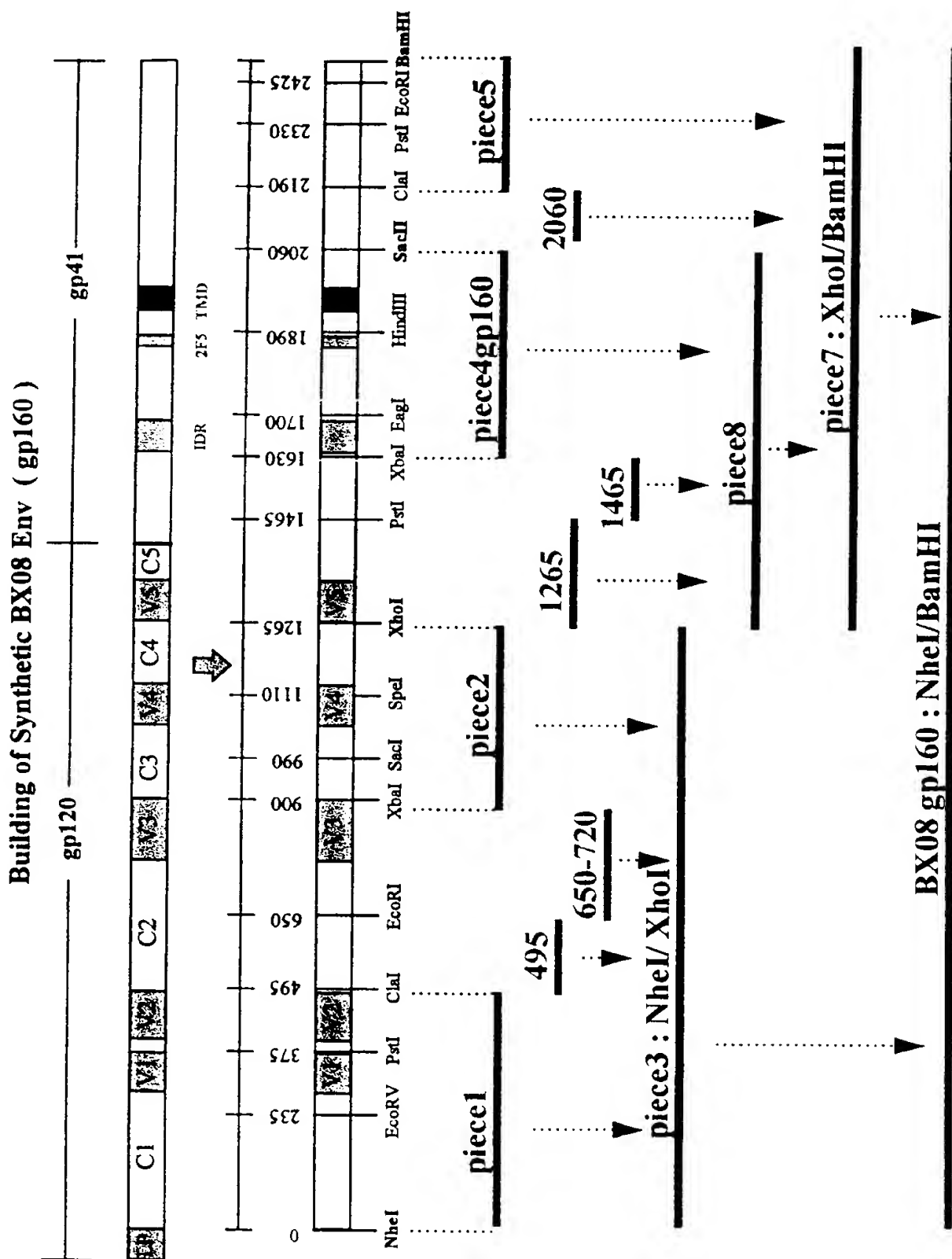


Fig. 6

STARTS: ATG

7/33

aa	Σ	codons
A Ala	GCX	GCT GCC GCG GCA
C Cys	TGY	TGT TGC
D Asp	GAY	GAT GAC
E Glu	GAR	GAG GAA
F Phe	TTY	TTT TTC
G Gly	GGX	GGT GGC GGG GGA
H His	CAY	CAT CAC
I Ile	ATH	ATT ATC ATA
K Lys	AAR	AAG AAA
L Leu	YTX	TTG TTA CTT CTC CTG CTA
M Met	ATG	ATG
N Asn	AAV	AAT AAC
P Pro	CCX	CCT CCC CCG CCA
Q Gln	CAR	CAG CAA
R Arg	MGX	CGT CGC CGG CGA AGG AGA
S Ser	WSX	TCT TCC TCG TCA AGT AGC
T Thr	ACX	ACT ACC ACG ACA
V Val	GTX	GTT GTC GTG GTA
W Trp	TGG	TGG
Y Tyr	TAY	TAT TAC
.	TRR	TGA TAG TAA
X ?		

		2nd					
5'		T	C	A	G	3'	
T		Phe	Ser	Tyr	Cys		T
		Phe	Ser	Tyr	Cys		C
		Leu	Ser	.	.		A
		Leu	Ser	.	Trp		G
C		Leu	Pro	His	Arg		T
		Leu	Pro	His	Arg		C
		Leu	Pro	Gln	Arg		A
		Leu	Pro	Gln	Arg		G
A		Ile	Thr	Asn	Ser		T
		Ile	Thr	Asn	Ser		C
		Ile	Thr	Lys	Arg		A
		Met	Thr	Lys	Arg		G
G		Val	Ala	Asp	Gly		T
		Val	Ala	Asp	Gly		C
		Val	Ala	Glu	Gly		A
		Val	Ala	Glu	Gly		G

Fig. 7

8/33

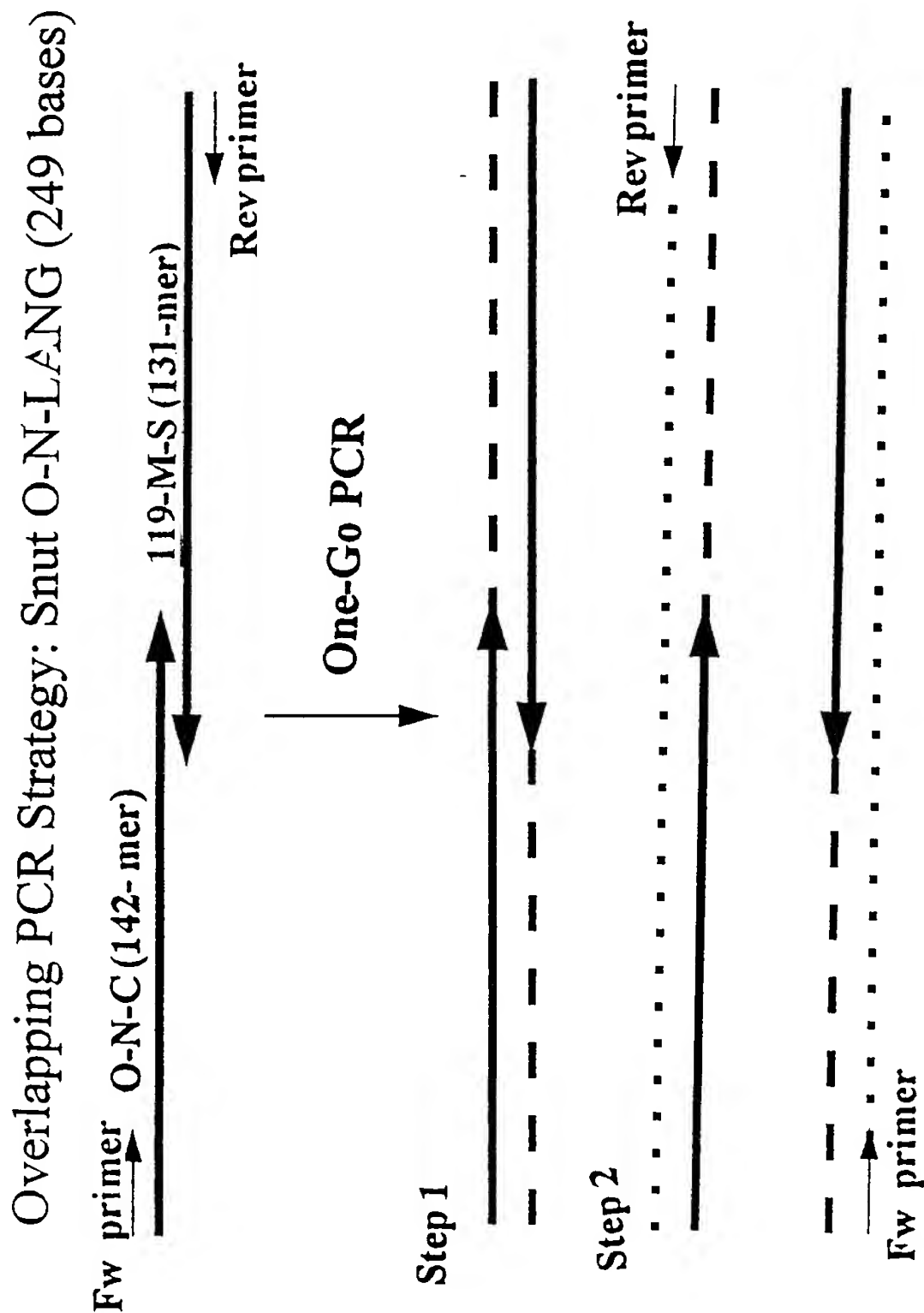


Fig. 8

9/33

PCR approach using conserved flanking sequences

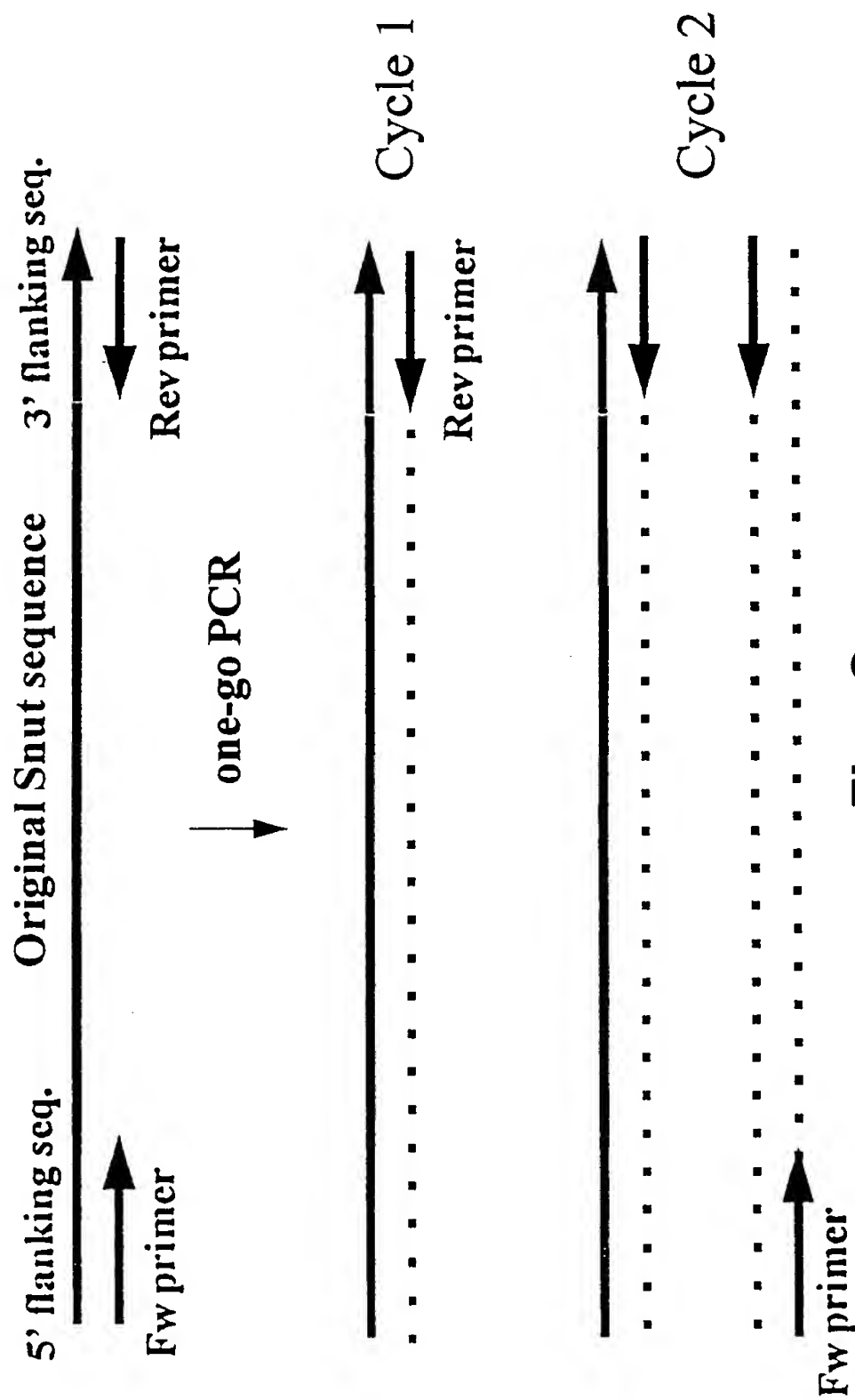


Fig. 9

10/33

Snut 1265 by minigene approach

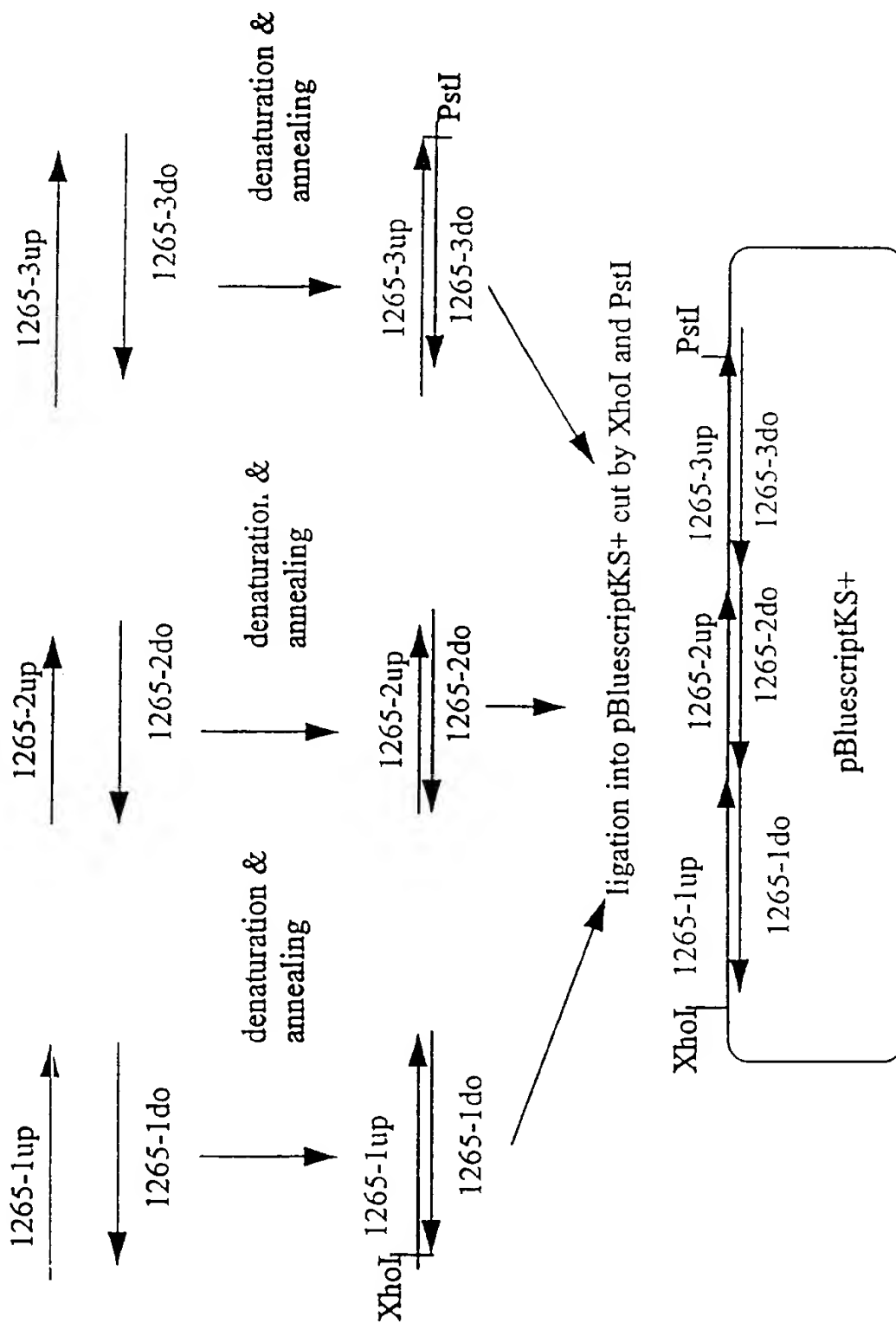


Fig. 10

11/33

Snut 1465- minigene approach

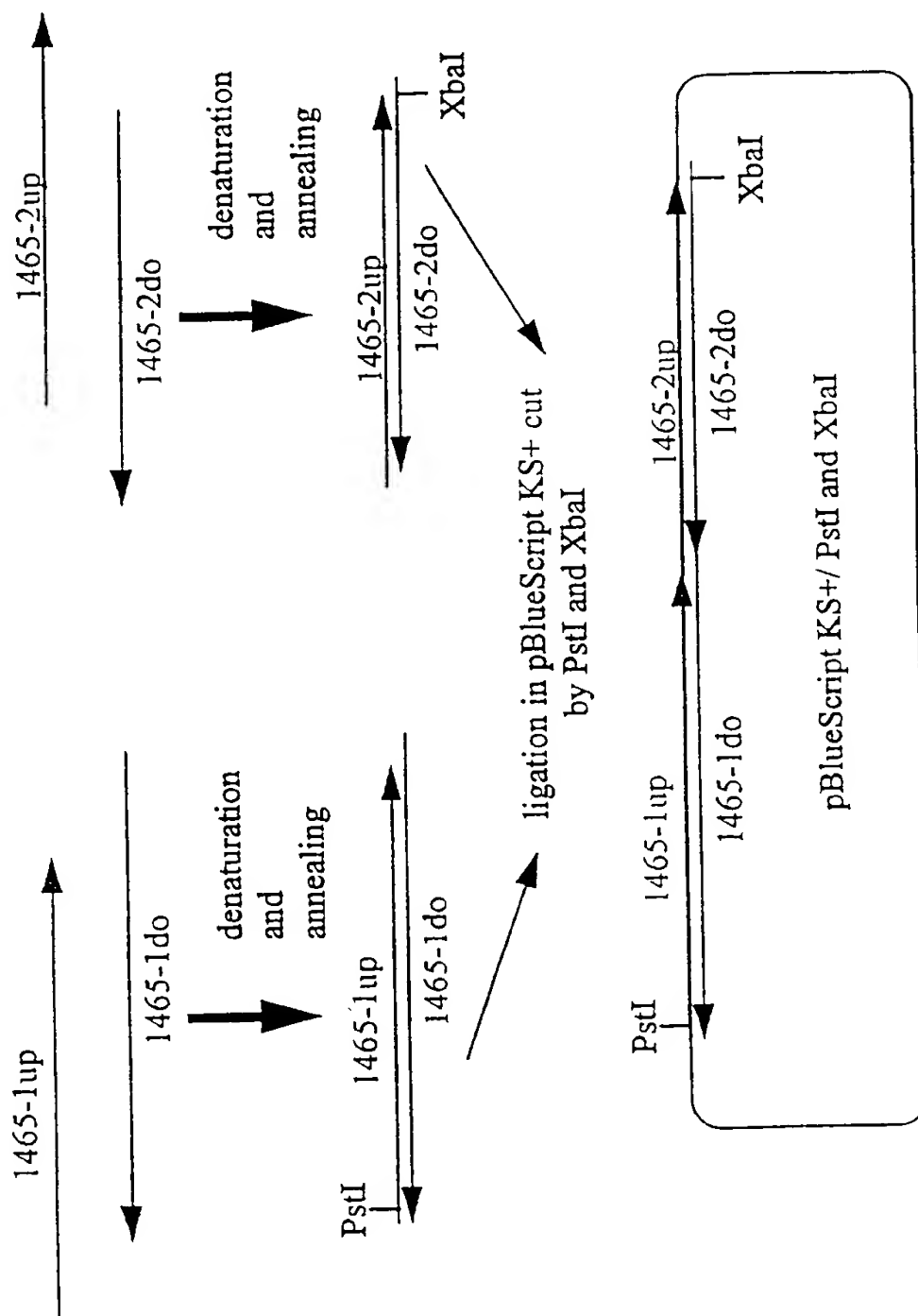


Fig. 11

12/33

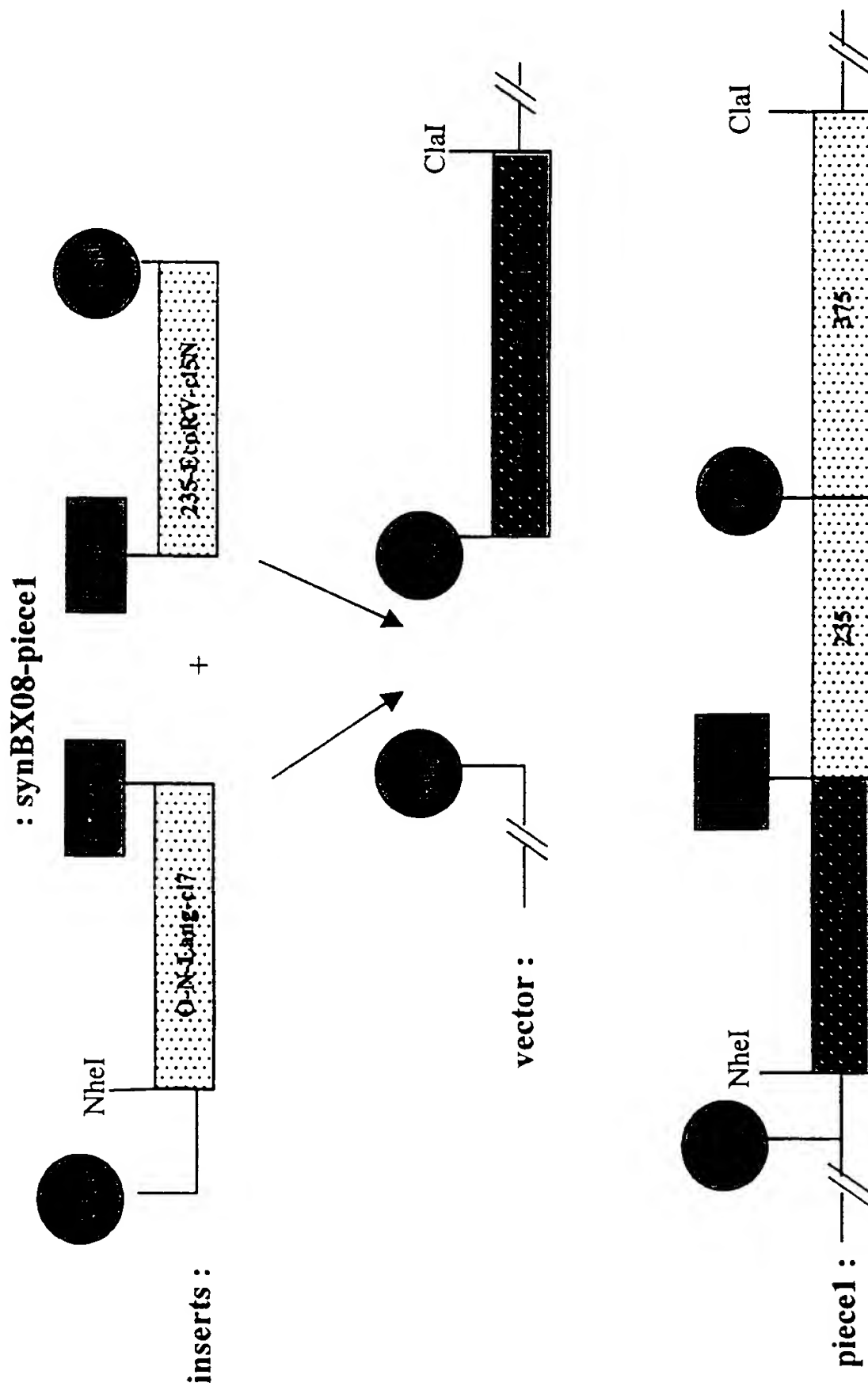


Fig. 12

13/33

synBX08-piece2

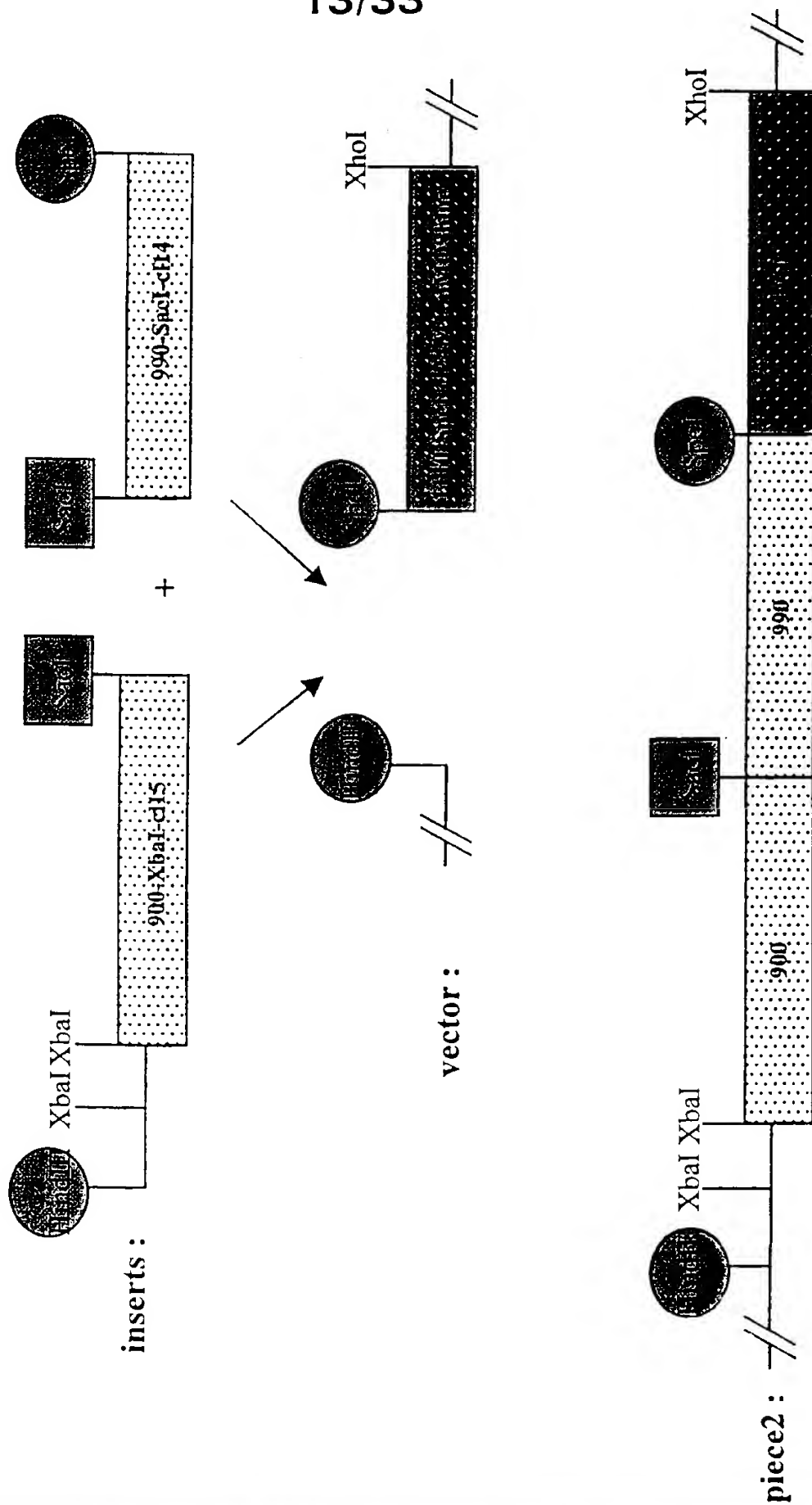


Fig. 13

14/33

synBX08-piece3

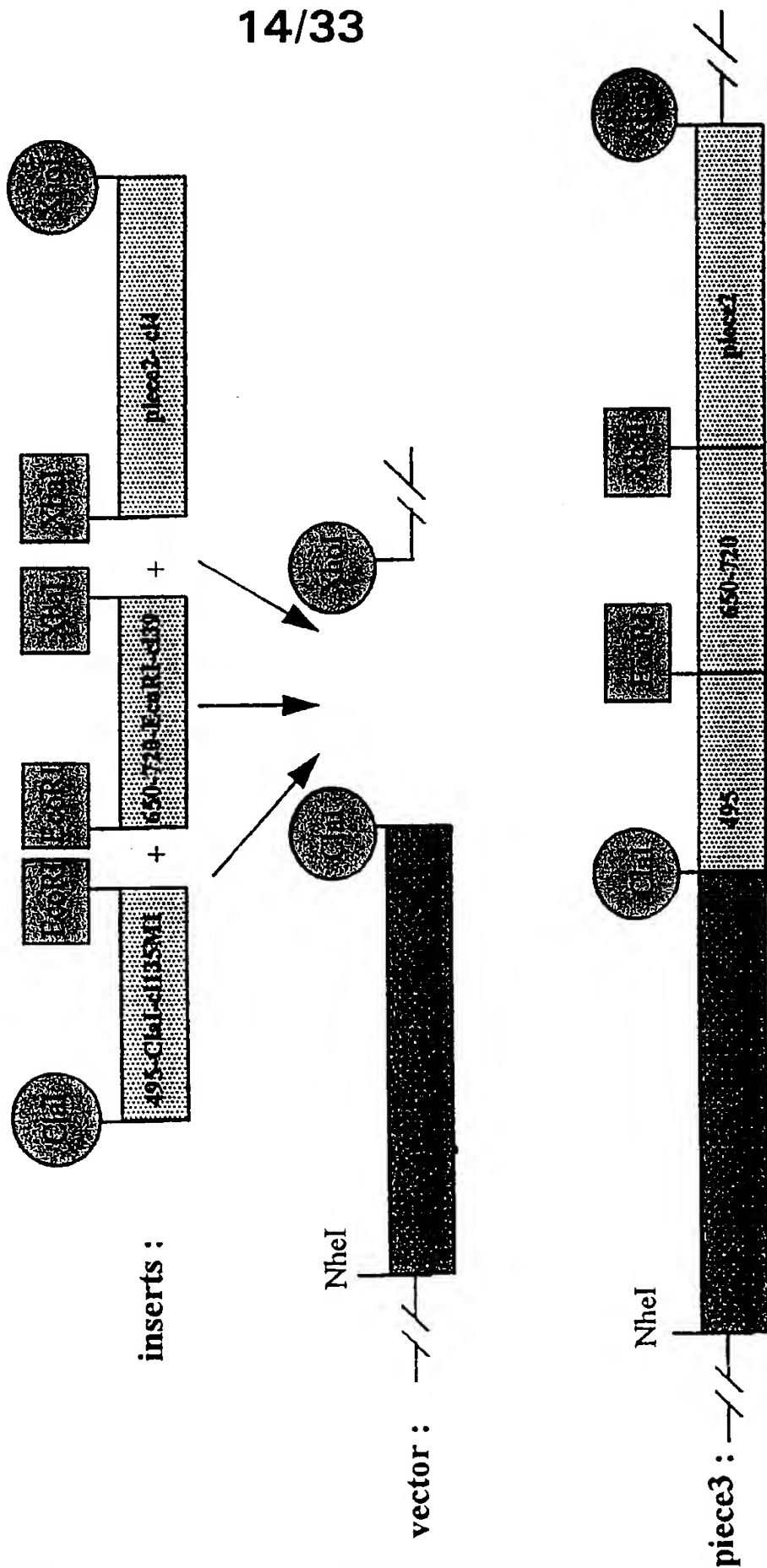
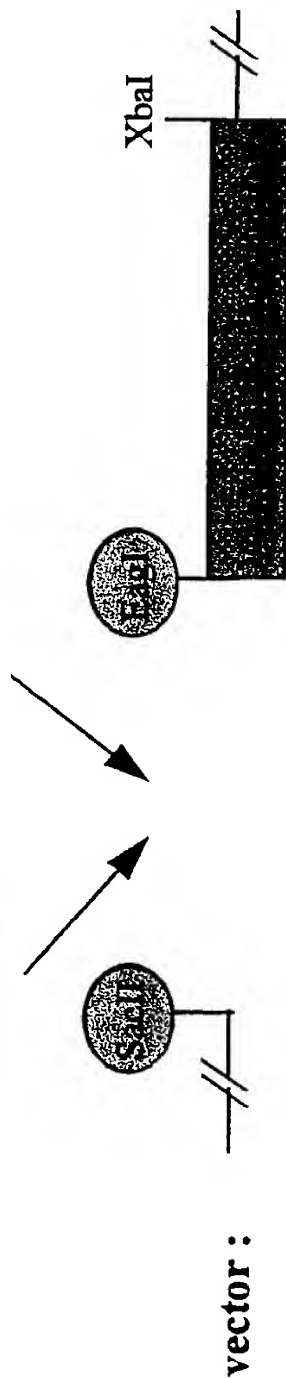
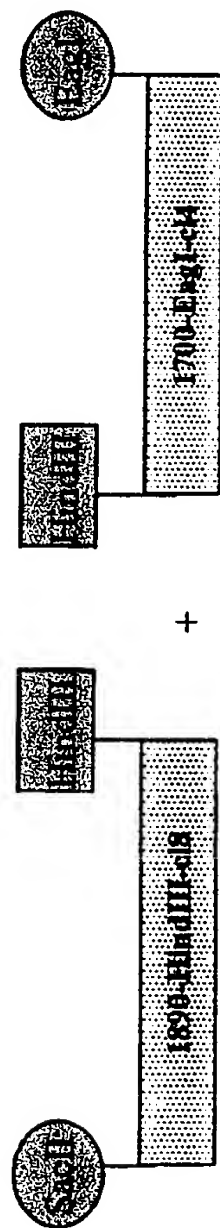


Fig. 14

synBX08-piece4gp160



vector :

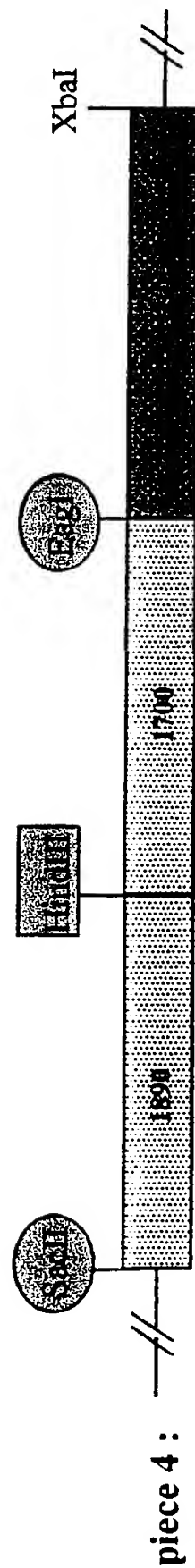


Fig. 15

16/33

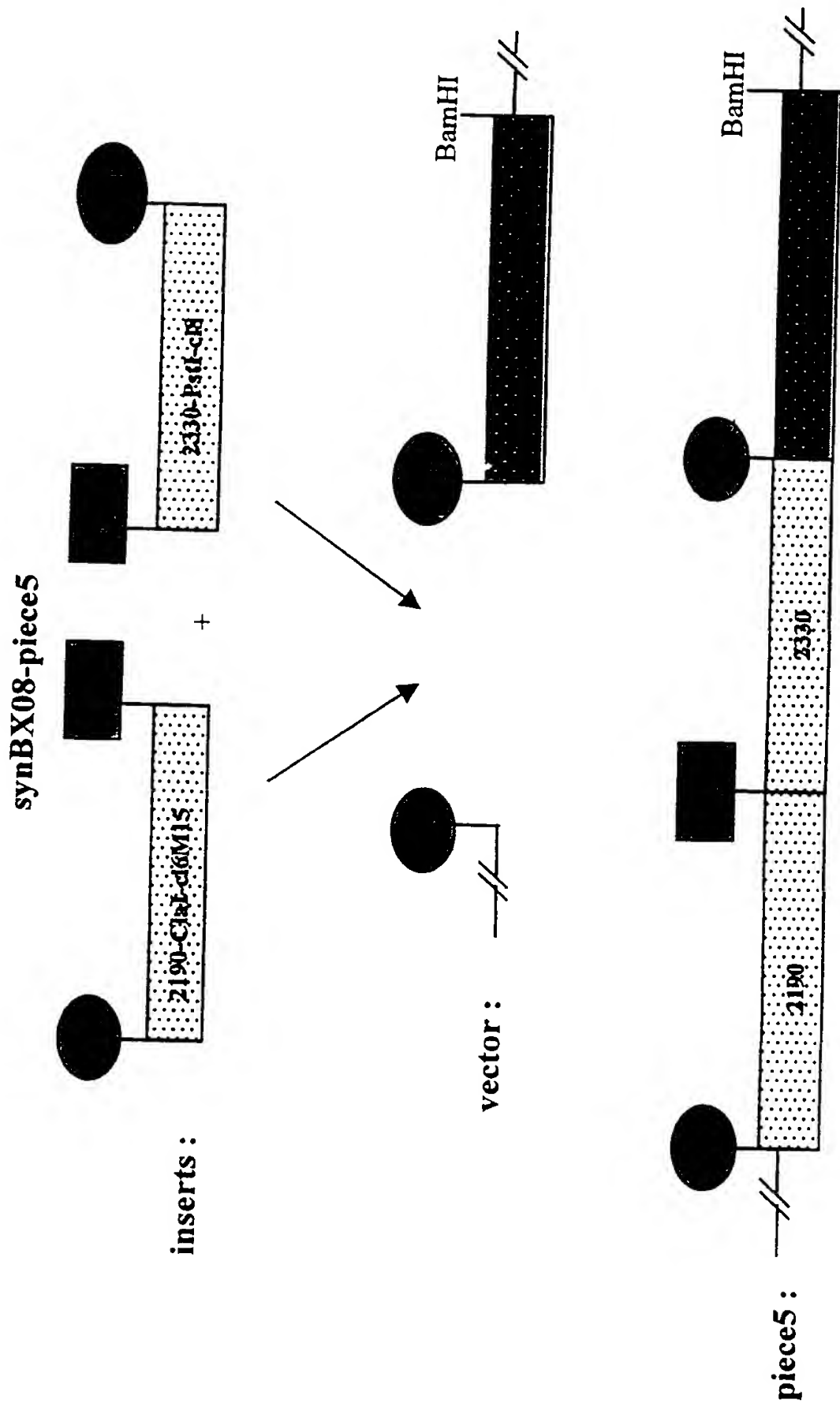


Fig. 16

17/33

Figure 17 : synBX08-piece8gp160

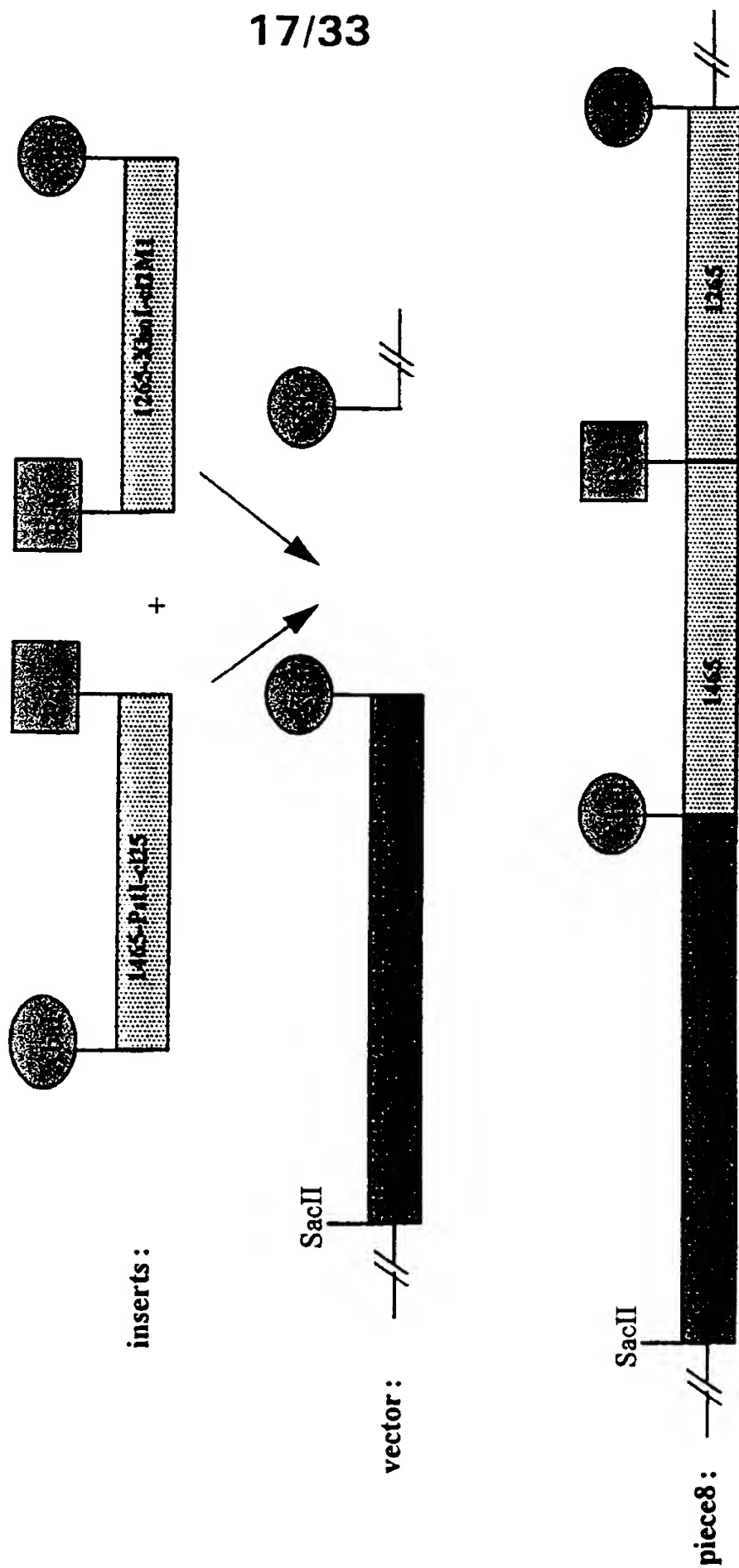


Fig. 17

synBX08-piece8-gp150

18/33

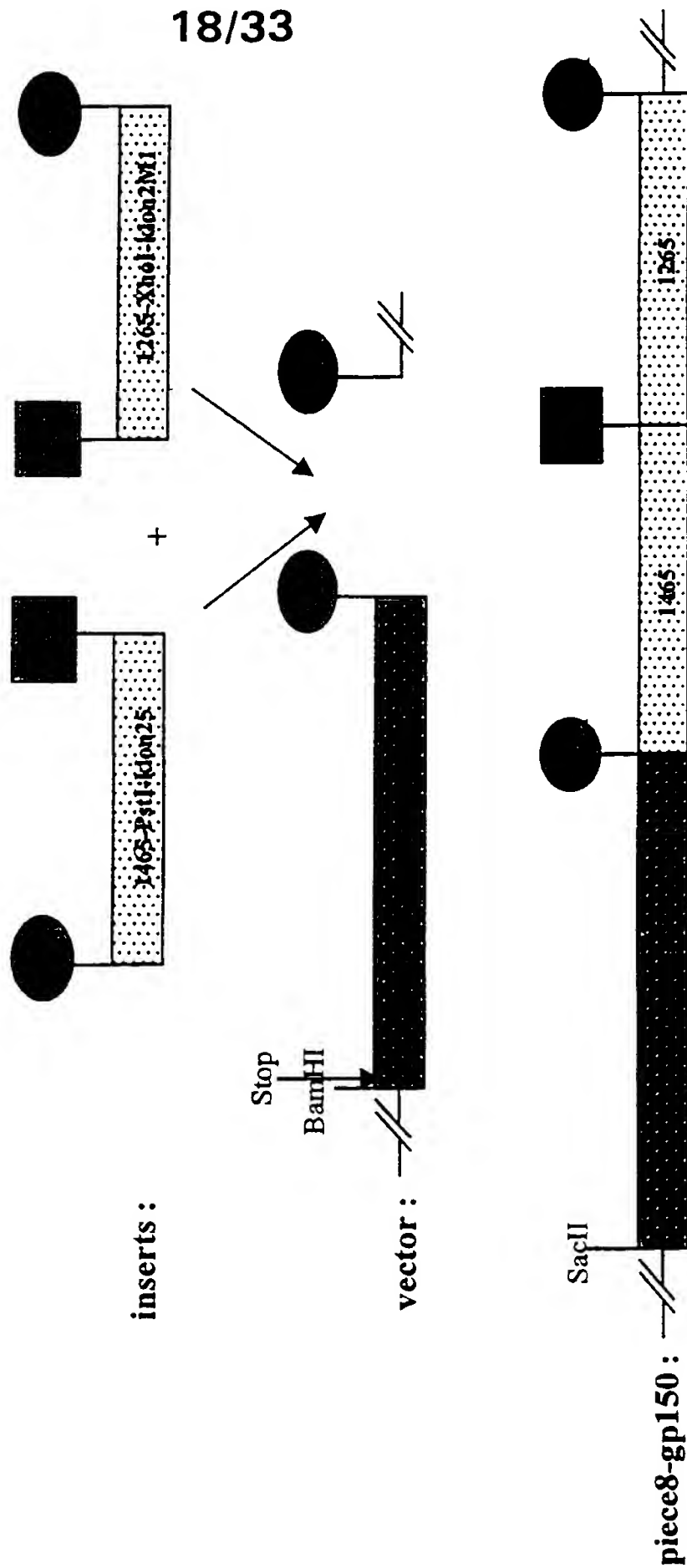


Fig. 18

synBX08-piece8-gp140

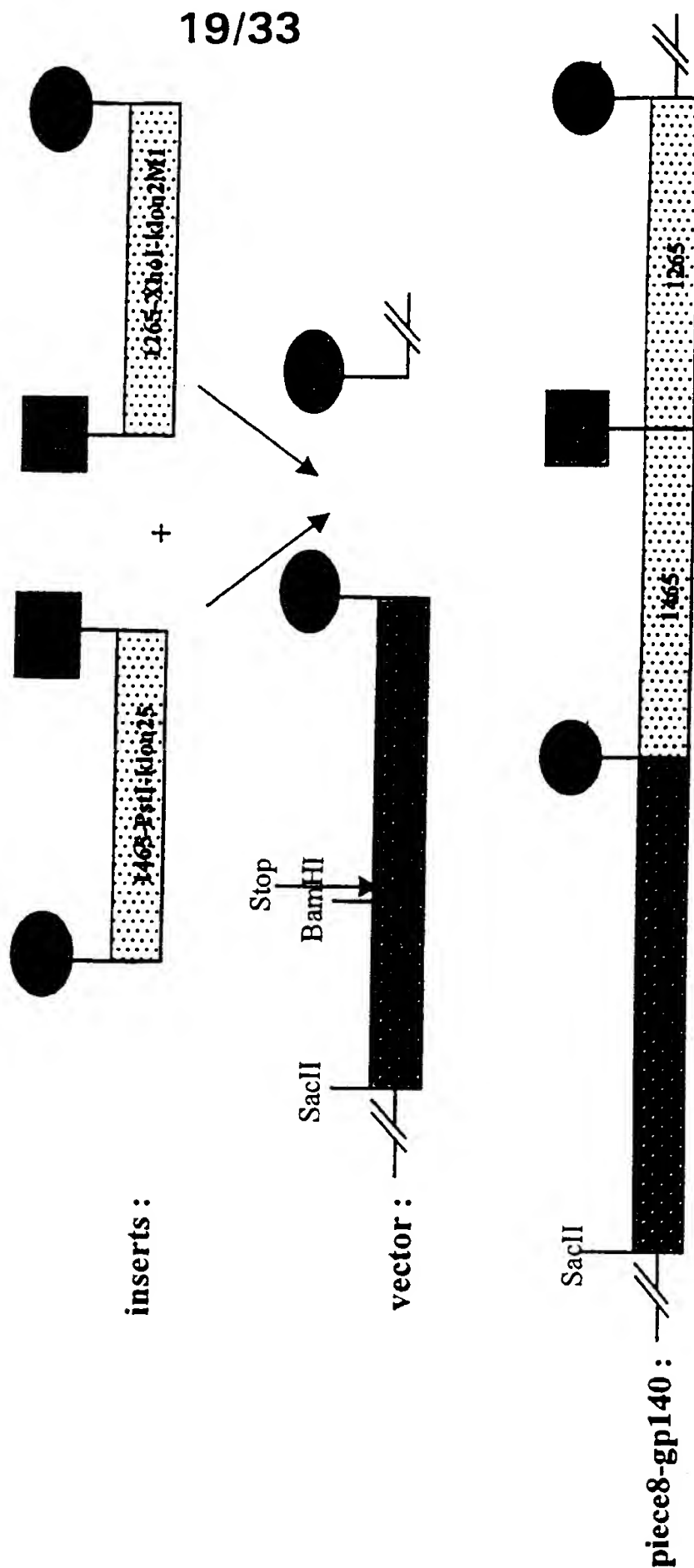


Fig. 19

Figure 20: synBX08-piece8-gp41

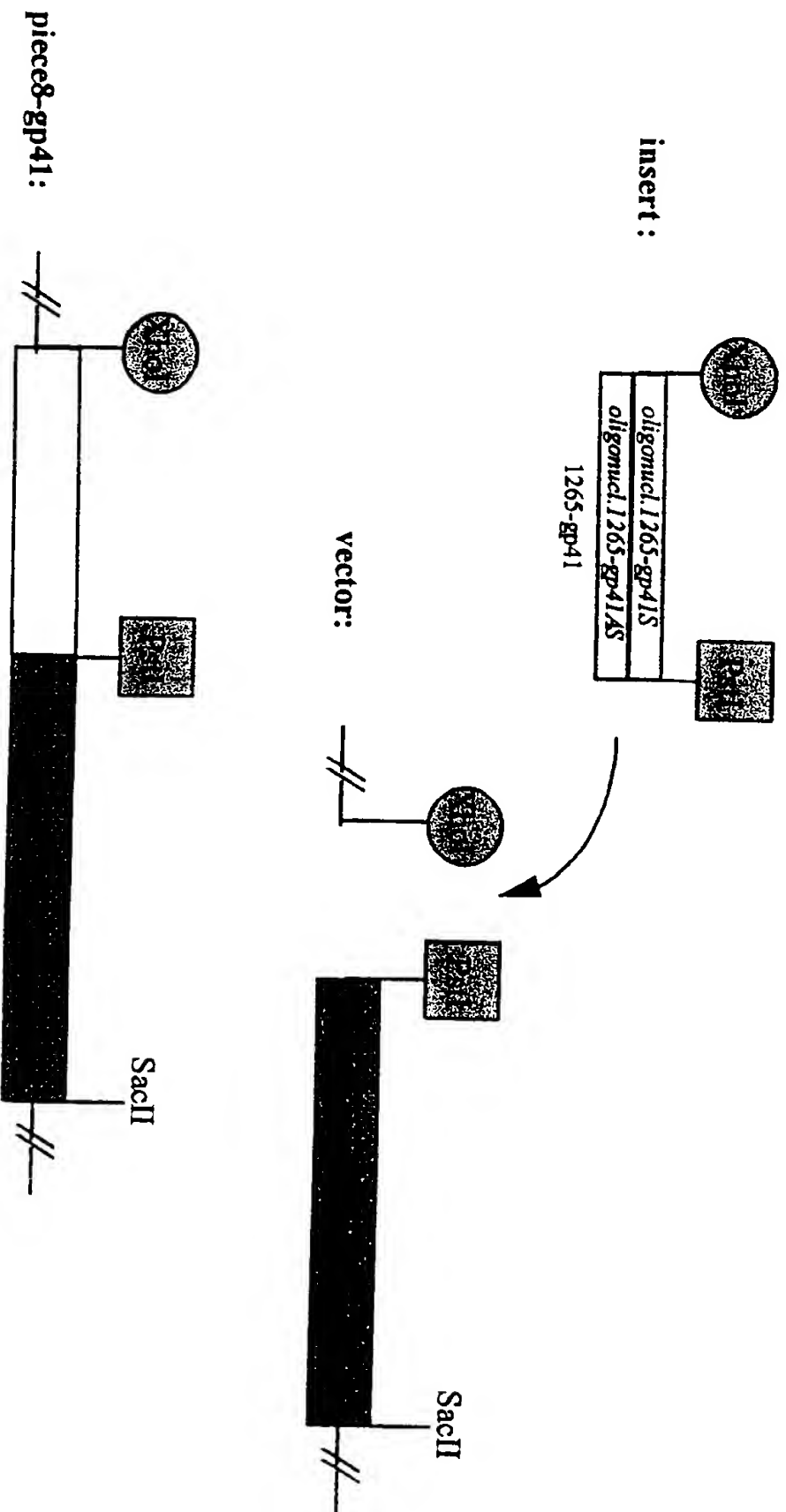


Fig. 20

synBX08-piece 7

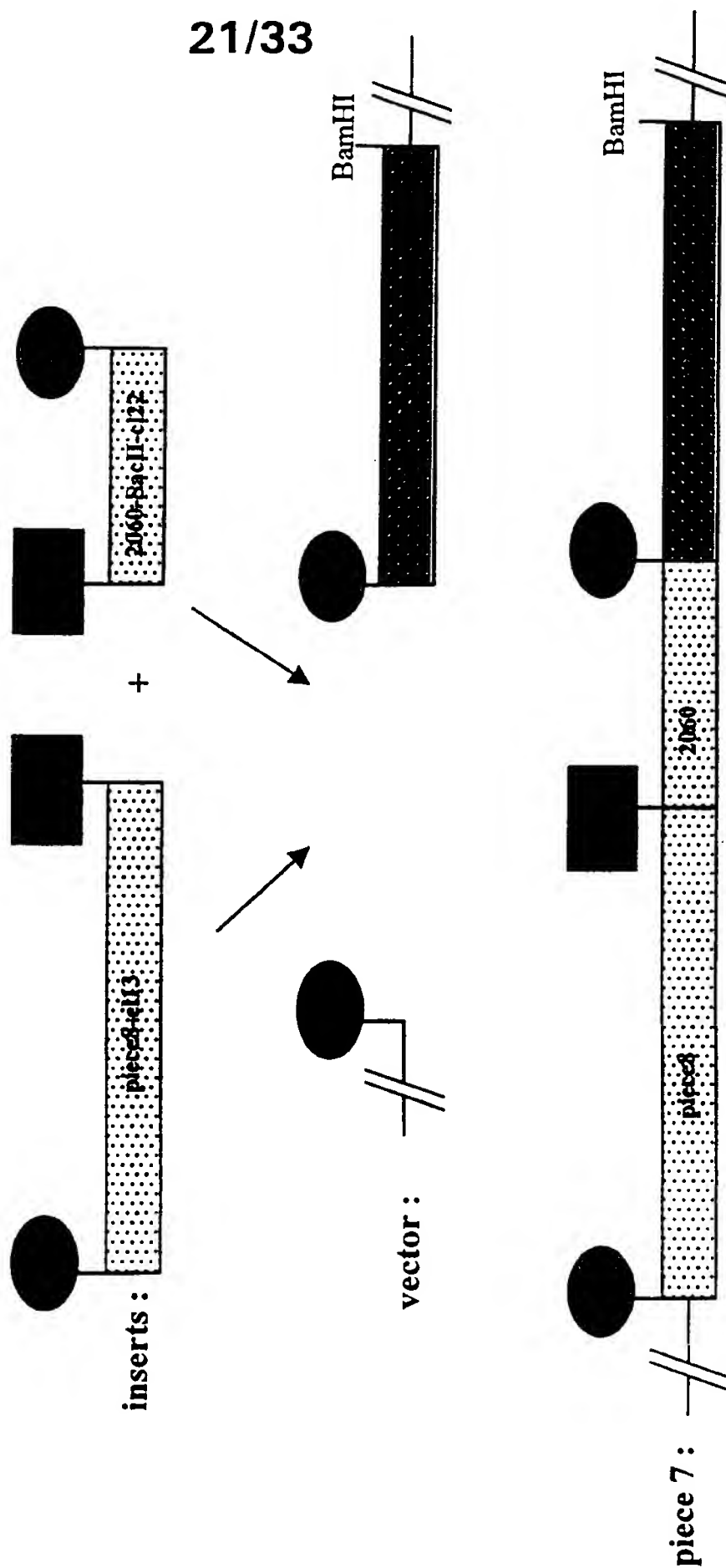


Fig. 21

22/33

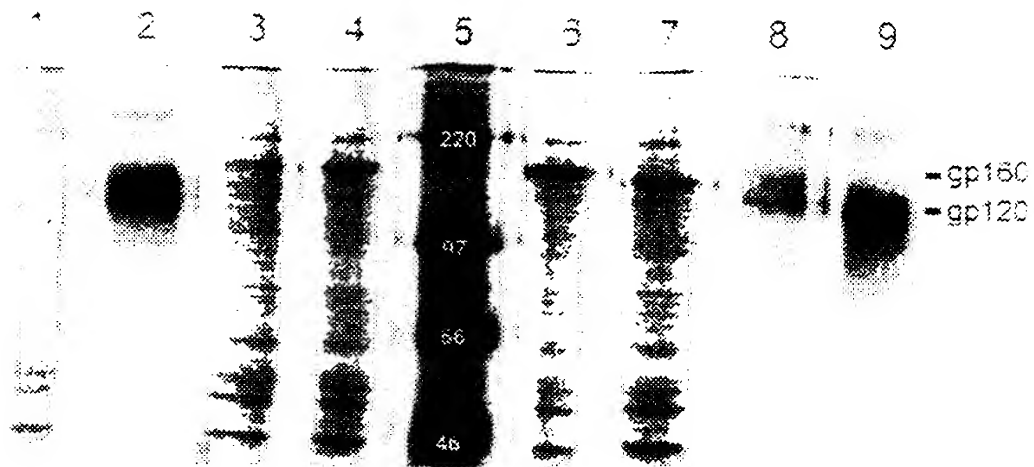


Fig. 22 A

23/33

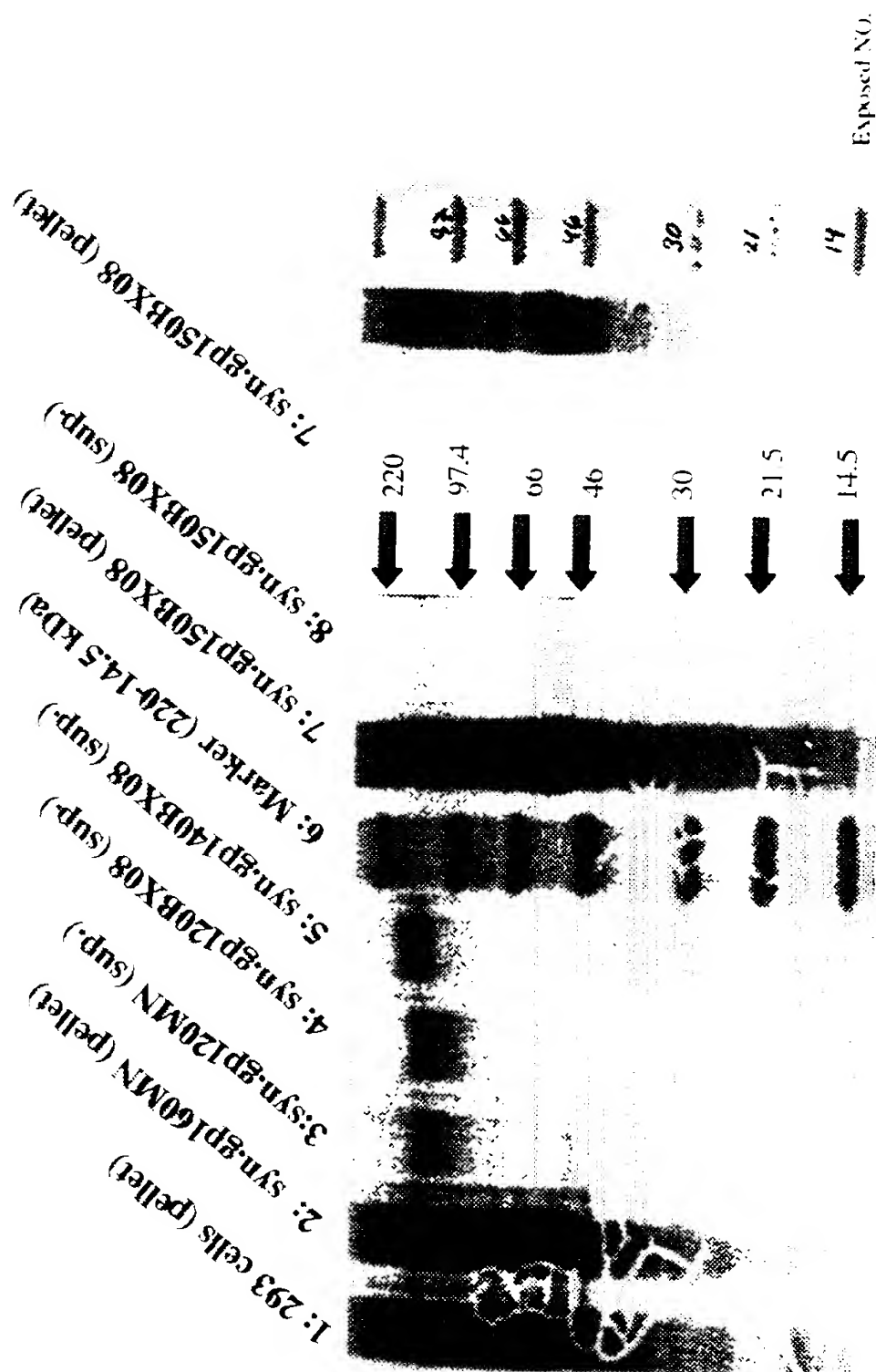


Fig. 22 B

24/33

Panel A



Fig. 22 C

25/33

Panel B

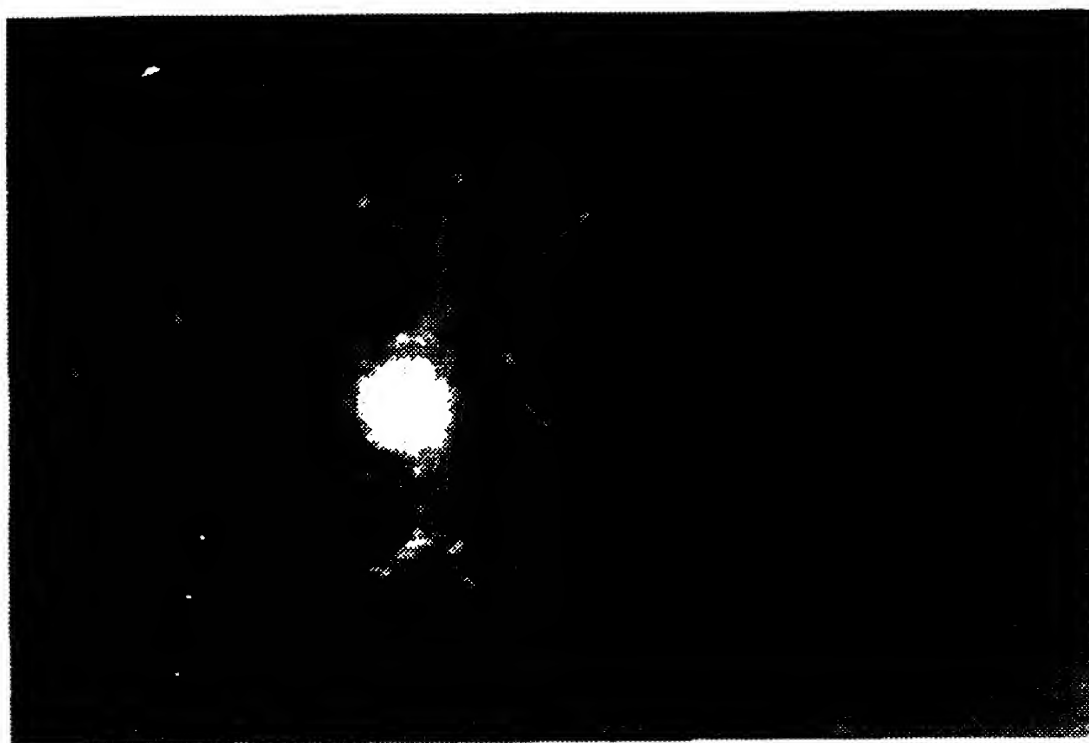


Fig. 22 C

26/33

Panel C

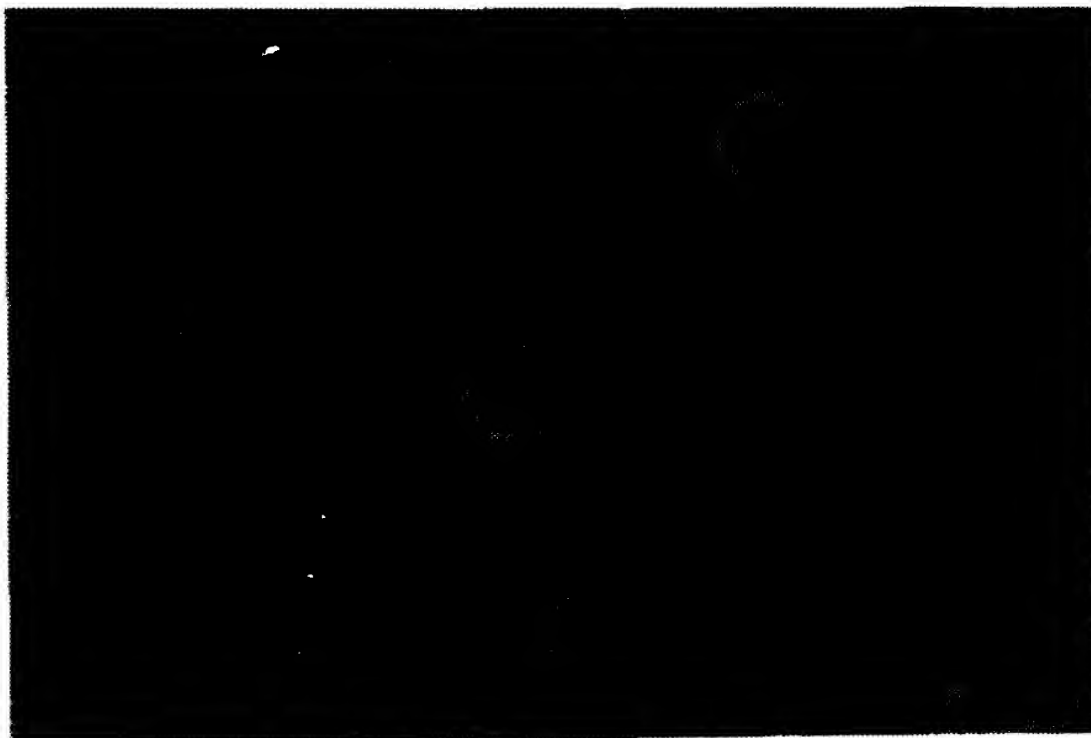


Fig. 22 C

27/33

IgG1 anti-V3 BX08 from Balb/c mice DNA vaccinated with envelope genes in WRG7079

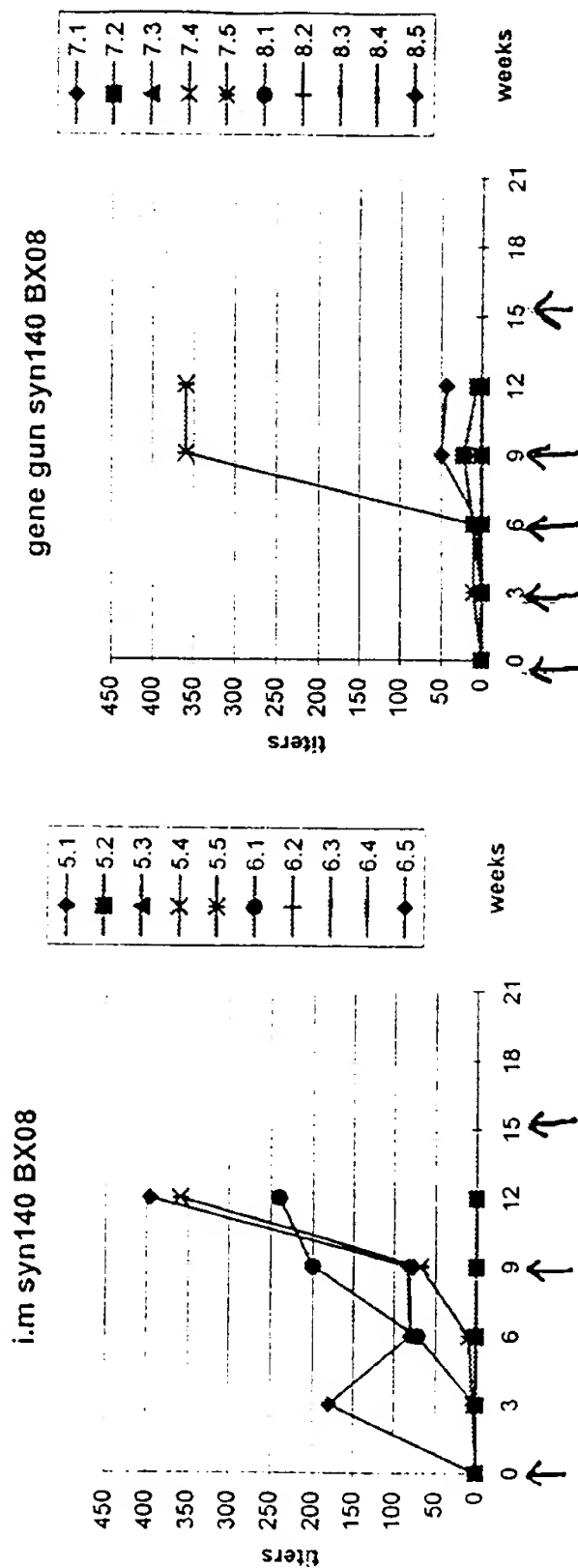


Fig. 23

28/33

C



Fig. 24

29/33

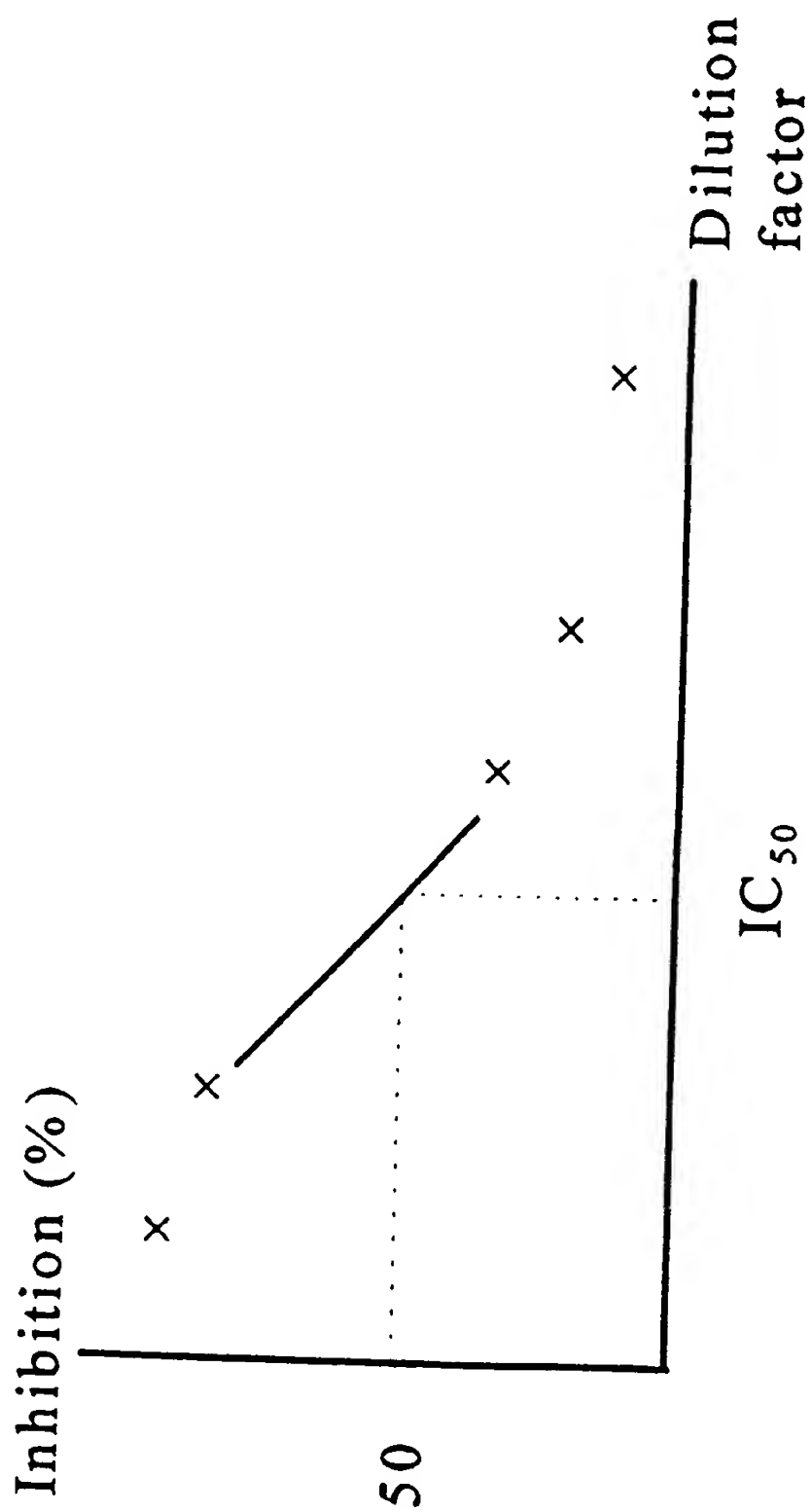


Fig. 25

30/33

Fig. 26 A CTL activity induced by
different synthetic DNA vaccines

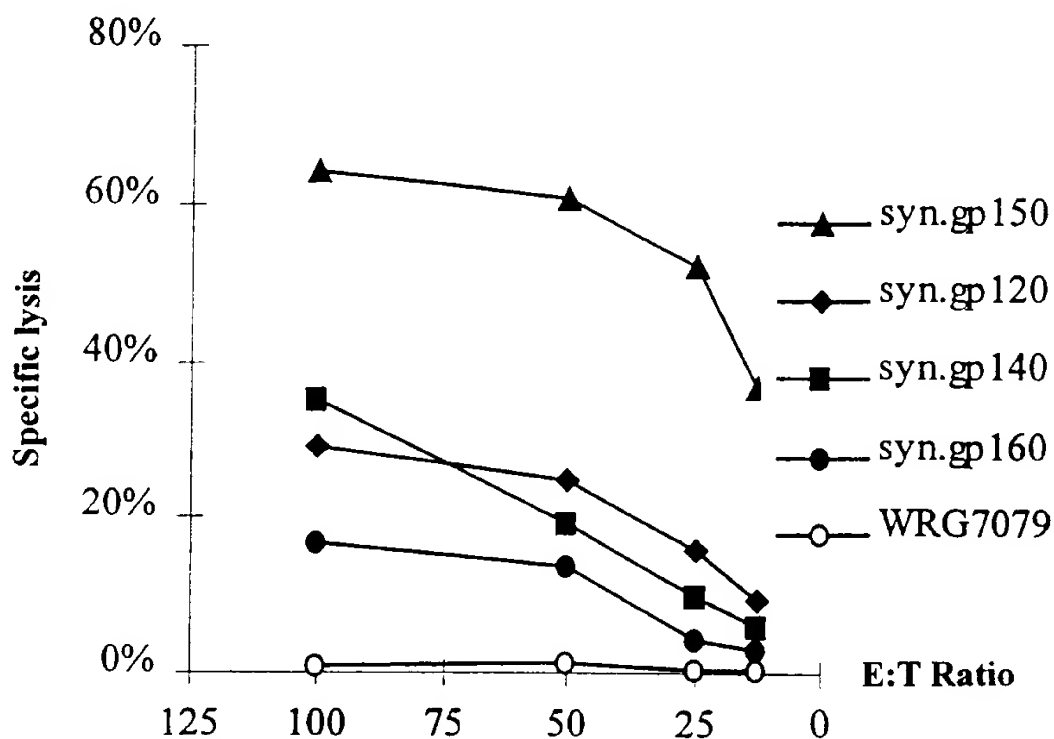
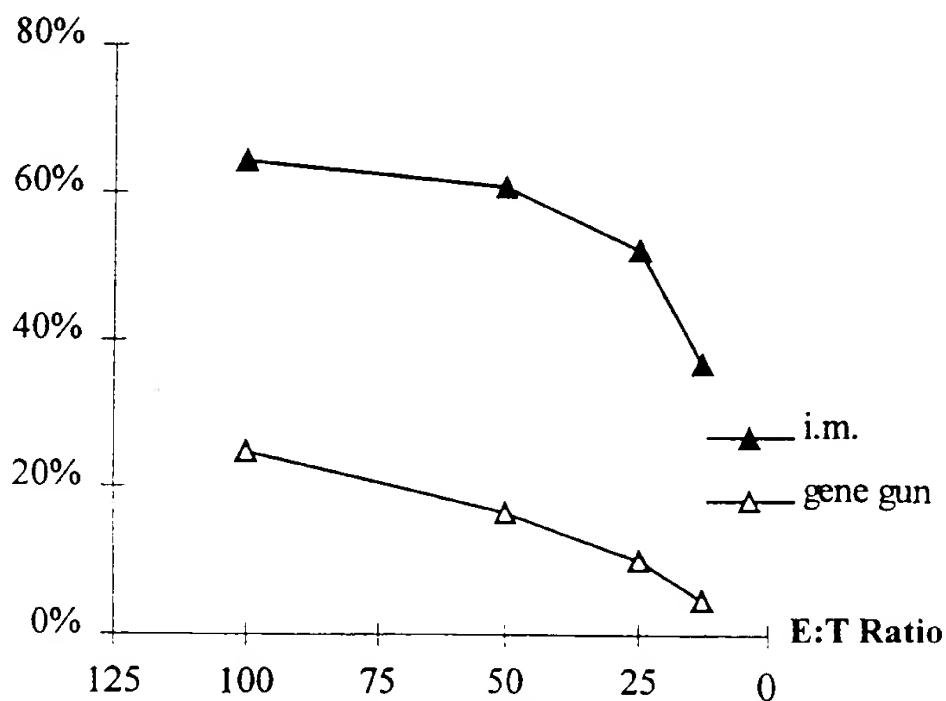


Fig. 26 B CTL activity induced by
different DNA delivery methods.

**Fig. 26**

31/33

		Percentage of antiserum positive to gp120 _{IIIb} and gp41 _{IIIb} in western blot assay		
Week		0	9	18
syn.gp120 _{BX08}	gp120	0	65	90
	gp41	0	0	35
syn.gp140 _{BX08}	gp120	0	65	100
	gp41	0	95	100
syn.gp150 _{BX08}	gp120	0	30	41
	gp41	0	41	53
syn.gp160 _{BX08}	gp120	0	32	50
	gp41	0	44	64
wt.gp160 _{BX08}	gp120	0	nd	53
	gp41	0	nd	48
wt.gp160 _{BX08} /pRev	gp120	0	nd	5
	gp41	0	nd	55

Fig. 27

32/33

Fig. 28 A

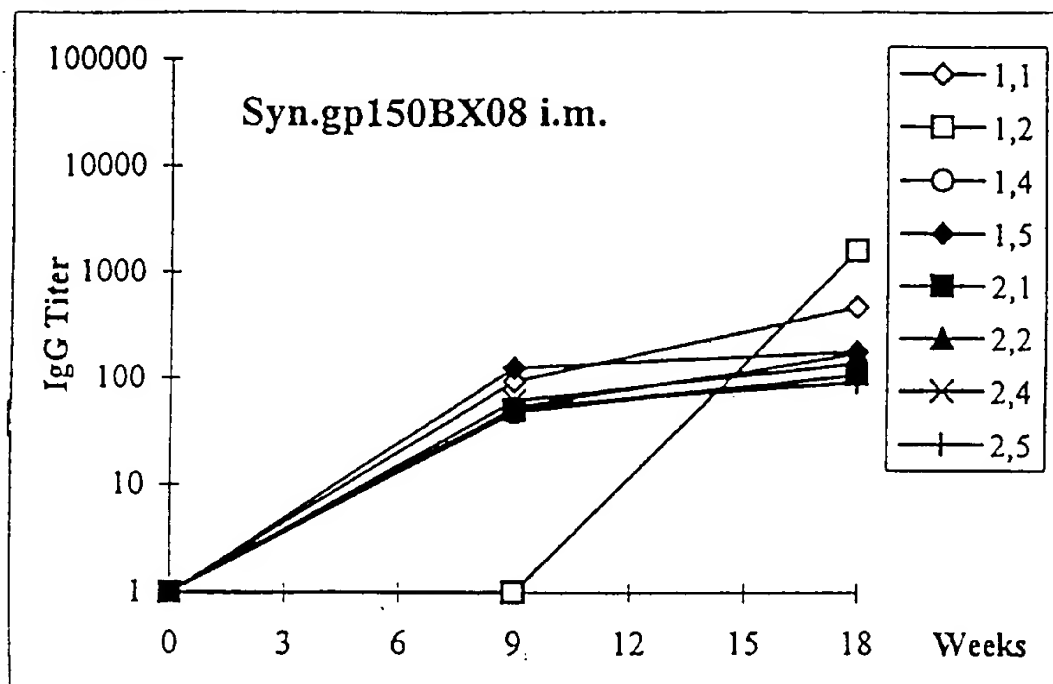


Fig. 28 B

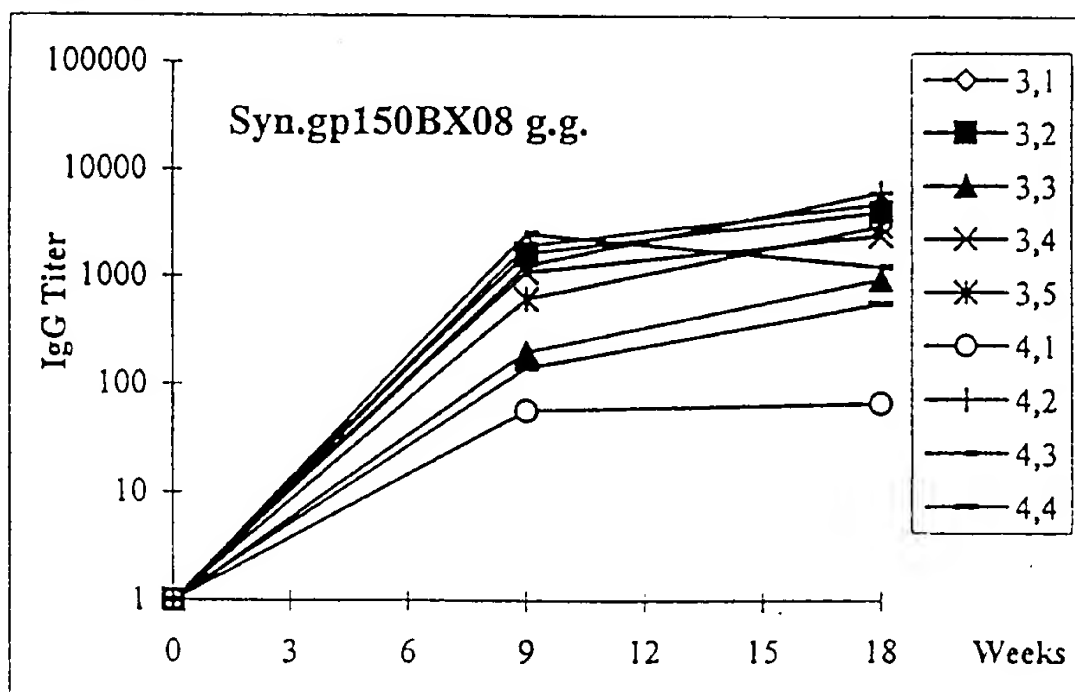


Fig. 28

33/33

Fig. 29 A

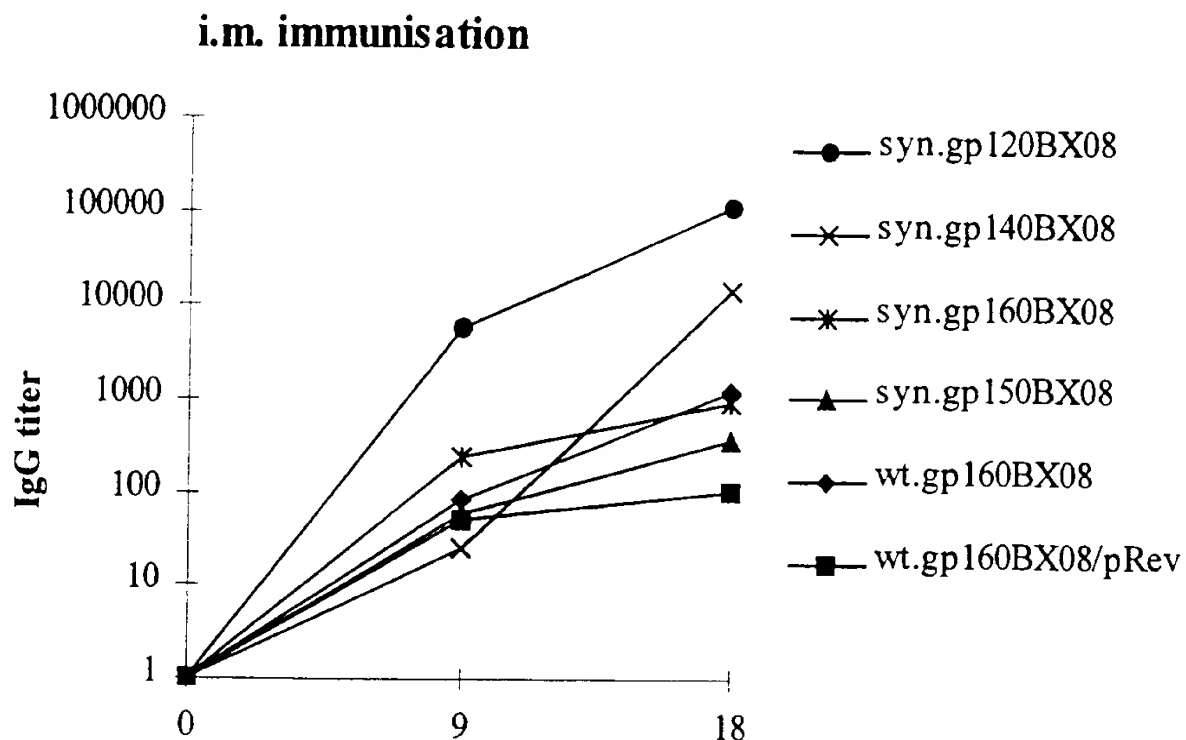


Fig. 29 B

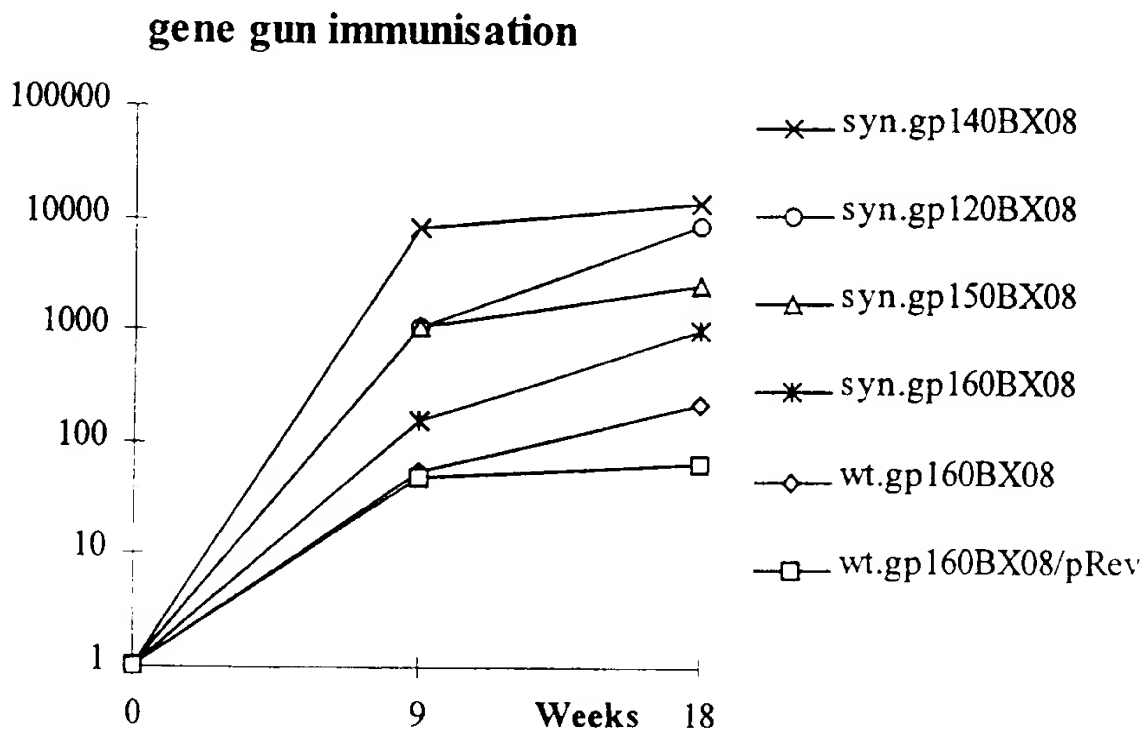


Fig. 29

SEQUENCE LISTING

*111> Statens Serum Institut

*120> Method for producing an nucleotide
sequence construct with optimised codons for an HIV envelope
based on a primary, clinical HIV isolate and the BX08
construct.

*130> 21924DK1

*160> 76

*170> FastSEQ for Windows Version 3.0

*210> 1

*211> 243

*212> DNA

*213> Artificial Sequence

*220>

*221> CDS

*222> (1)...(243)

*400> 1

gct	agc	gag	gcc	gac	cgc	ctg	tgg	gtg	acc	gtg	tac	tac	ggc	gtg	ccc	48
Ala	Ser	Ala	Ala	Asp	Arg	Leu	Trp	Val	Thr	Val	Tyr	Tyr	Gly	Val	Pro	
1				5					10					15		

gtg	tgg	aag	gac	gcc	acc	acc	acc	ctg	ttc	tgc	gcc	agc	gac	gcc	aag	96
Val	Trp	Lys	Asp	Ala	Thr	Thr	Thr	Leu	Phe	Cys	Ala	Ser	Asp	Ala	Lys	
			20					25						30		

gcc	tac	gac	acc	gag	gtg	cac	aac	gtg	tgg	gcc	acc	cac	gcg	tgc	gtg	144
Ala	Tyr	Asp	Thr	Glu	Val	His	Asn	Val	Trp	Ala	Thr	His	Ala	Cys	Val	
			35				40					45				

ccc	acc	gac	ccc	aac	ccc	cag	gag	gtg	gtg	ctg	ggc	aac	gtg	acc	gag	192
Pro	Thr	Asp	Pro	Asn	Pro	Gln	Glu	Val	Val	Leu	Gly	Asn	Val	Thr	Glu	
			50				55				60					

aac	ttc	aac	atg	ggc	aag	aac	aac	atg	gtg	gag	cag	atg	cac	gag	gat	240
Asn	Phe	Asn	Met	Gly	Lys	Asn	Asn	Met	Val	Glu	Gln	Met	His	Glu	Asp	
65					70				75				80			

atc																243
Ile																

*210> 2

*211> 81

*212> PRT

*213> Artificial Sequence

*400> 2

Ala	Ser	Ala	Ala	Asp	Arg	Leu	Trp	Val	Thr	Val	Tyr	Tyr	Gly	Val	Pro
1				5					10					15	

Val	Trp	Lys	Asp	Ala	Thr	Thr	Thr	Leu	Phe	Cys	Ala	Ser	Asp	Ala	Lys
			20					25					30		
Ala	Tyr	Asp	Thr	Glu	Val	His	Asn	Val	Trp	Ala	Thr	His	Ala	Cys	Val
		35					40					45			
Pro	Thr	Asp	Pro	Asn	Pro	Gln	Glu	Val	Val	Leu	Gly	Asn	Val	Thr	Glu
	50					55					60				
Asn	Phe	Asn	Met	Gly	Lys	Asn	Asn	Met	Val	Glu	Gln	Met	His	Glu	Asp
65					70					75					80
Ile															

4210: 3

4211: 143

4212: DNA

4213: Artificial Sequence

4220:

4221: CDS

4222: (1)...(143)

4400: 3

gat	att	ata	agg	ctg	tgg	gac	cag	agc	ctg	aag	ccc	tgc	gtg	aag	ctg	48
Asp	Ile	Ile	Ser	Leu	Trp	Asp	Gln	Ser	Leu	Lys	Pro	Cys	Val	Lys	Leu	
1				5					10				15			

acc	ccc	ctg	tgc	gtg	acc	ctg	aac	tgc	acc	aag	ctg	aag	aac	agc	acc	96
Thr	Pro	Leu	Cys	Val	Thr	Leu	Asn	Cys	Thr	Lys	Leu	Lys	Asn	Ser	Thr	
			20					25					30			

gac	acc	aac	aac	acc	cgc	tgg	ggc	acc	cag	gag	atg	aag	aac	tgc	ag	143
Asp	Thr	Asn	Asn	Thr	Arg	Trp	Gly	Thr	Gln	Glu	Met	Lys	Asn	Cys		
		35					40					45				

4410: 4

4411: 47

4412: PPT

4413: Artificial Sequence

4400: 4

Asp	Ile	Ile	Ser	Leu	Trp	Asp	Gln	Ser	Leu	Lys	Pro	Cys	Val	Lys	Leu
1				5					10				15		
Thr	Pro	Leu	Cys	Val	Thr	Leu	Asn	Cys	Thr	Lys	Leu	Lys	Asn	Ser	Thr
			20					25					30		
Asp	Thr	Asn	Asn	Thr	Arg	Trp	Gly	Thr	Gln	Glu	Met	Lys	Asn	Cys	
		35					40					45			

4410: 5

4411: 132

4412: DNA

4413: Artificial Sequence

4420:

4421: CDS

4422: (1)...(132)

4400: 5

ctg	cag	ctt	caa	cat	cag	cac	cag	cgt	ggc	caa	caa	gat	gaa	ggc	cga
Leu	Gln	Leu	Gln	His	Gln	His	Gln	Arg	Ala	Gln	Gln	Asp	Glu	Ala	Arg

```

1           5           10           15
gta cga cct gtt cta sag cct gga cat cgt gcc cat cga caa cga caa      96
Val Arg Pro Val Leu Gln Pro Gly His Arg Ala His Arg Gln Arg Gln
          20          25          30

cac cag cta cgg cct gcg cag ctg caa cac atc gat      132
His Gln Leu Pro Pro Ala Gln Leu Gln His Ile Asp
          35          40

<210> 6
<211> 44
<212> PRT
<213> Artificial Sequence

<400> 6
Leu Gln Leu Gln His Gln His Gln Arg Ala Gln Gln Asp Glu Ala Arg
1           5           10           15
Val Arg Pro Val Leu Gln Pro Gly His Arg Ala His Arg Gln Arg Gln
          20          25          30
His Gln Leu Pro Pro Ala Gln Leu Gln His Ile Asp
          35          40

<210> 7
<211> 161
<212> DNA
<213> Artificial Sequence

<220>
<221> CDS
<222> (1)...(161)

<400> 7
atc gat caa cac cca ggc ctg ccc caa ggt gag ctt cga gcc cat ccc      48
Ile Asp His His Pro Gly Leu Pro Gln Gly Glu Leu Arg Ala His Pro
1           5           10           15

cat cca ctt ctg cgc ccc cgc cgg ctt cgc cat cct gaa gtg caa caa      96
His Pro Leu Leu Arg Pro Arg Arg Leu Arg His Pro Glu Val Gln Gln
          20          25          30

caa gag ctt caa cgg cac cgg ccc ctg cac caa cgt gag cac cgt gca      144
Gln Asp Leu Gln Arg His Arg Pro Leu His Gln Arg Glu His Arg Ala
          35          40          45

gtg cac cca cgg aat tc      161
Val His Pro Arg Asn
          50

```

```

<210> 8
<211> 53
<212> PRT
<213> Artificial Sequence

```

```

<400> 8
Ile Asp His His Pro Gly Leu Pro Gln Gly Glu Leu Arg Ala His Pro
1           5           10           15

```

His Pro Leu Leu Arg Pro Arg Arg Leu Arg His Pro Glu Val Gln Gln
 20 25 30
 Gln Asp Leu Gln Arg His Arg Pro Leu His Gln Arg Glu His Arg Ala
 35 40 45
 Val His Pro Arg Asn
 50

<210> 9
 <211> 254
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> CDS
 <222> 1... (254)

<400> 9
 gaa tta gaa cag tgg tga gca ccc agc tgc tgc tga acg gca gcc tgg 48
 Glu Phe Ala Pro Trp * Ala Pro Ser Cys Cys * Thr Ala Ala Trp
 1 5 10
 cag agg agt agt tgg tga tca gat ctg aga act tca cca aca acg cca 96
 Pro Arg Arg Arg Trp * Ser Asp Leu Arg Thr Ser Pro Thr Thr Pro
 15 20 25
 aga cca tca tgg tgc agc tga acg aga gcg tgg aga tca act gca ccc 144
 Arg Pro Ser Ser Cys Ser * Thr Arg Ala Trp Arg Ser Thr Ala Pro
 30 35 40
 gcc cca aca aba aca ccc gca aga gca tcc aca tgc gcc ctg gcc gcg 192
 Ala Pro Thr Thr Thr Pro Ala Arg Ala Ser Thr Ser Ala Leu Ala Ala
 45 50 55 60
 cct tct aca cca ccg gcg aca tca tgc gcg aca tcc gcc agg ccc act 240
 Pro Ser Thr Pro Pro Ala Thr Ser Ser Ala Thr Ser Ala Arg Pro Thr
 65 70 75
 gca aca tct cta ga 254
 Ala Thr Ser Leu
 80

<210> 10
 <211> 80
 <212> PRT
 <213> Artificial Sequence

<400> 10
 Glu Phe Ala Pro Trp Ala Pro Ser Cys Cys Thr Ala Ala Trp Pro Arg
 1 5 10 15
 Arg Arg Trp Ser Asp Leu Arg Thr Ser Pro Thr Thr Pro Arg Pro Ser
 20 25 30
 Ser Cys Ser Thr Arg Ala Trp Arg Ser Thr Ala Pro Ala Pro Thr Thr
 35 40 45
 Thr Pro Ala Arg Ala Ser Thr Ser Ala Leu Ala Ala Pro Ser Thr Pro
 50 55 60
 Pro Ala Thr Ser Ser Ala Thr Ser Ala Arg Pro Thr Ala Thr Ser Leu
 65 70 75 80

<210> 11
 <211> 92
 <11> DNA
 <12> Artificial Sequence

<20>
 <21> CDS
 <22> (1)...(92)

<400> 11
 tct agt acc aac tgg acc aac acc ctg aag cgc gtg gcc gag aag ctg 48
 Ser Arg Thr Asn Trp Thr Asn Thr Leu Lys Arg Val Ala Glu Lys Leu
 5 10 15
 cgc gag aac ttc aac aac acc acc atc gtg ttc aac cag agc tc 92
 Arg Glu Lys Phe Asn Asn Thr Thr Ile Val Phe Asn Gln Ser
 20 25 30

<11> 12
 <11> 30
 <12> PRT
 <13> Artificial Sequence

<400> 12
 Ser Arg Thr Asn Trp Thr Asn Thr Leu Lys Arg Val Ala Glu Lys Leu
 1 5 10 15
 Arg Glu Lys Phe Asn Asn Thr Thr Ile Val Phe Asn Gln Ser
 20 25 30

<20> 13
 <21> 130
 <12> DNA
 <13> Artificial Sequence

<20>
 <21> CDS
 <22> (1)...(130)

<400> 13
 gag ctg ggg cgg cga ccc cga gat cgt gat gca cag ctt caa ctg cgg 48
 Glu Leu Arg Arg Arg Pro Arg Asp Arg Asp Ala Gln Leu Gln Leu Arg
 1 5 10 15
 cgg cga gtt ctt cta ctg caa cac cac cca gct gtt caa cag cac ctg 96
 Arg Arg Val Leu Leu Leu Gln His His Pro Ala Val Gln Gln His Leu
 20 25 30
 gaa cga gag caa cag cga ggg caa cat cac tag t 130
 Glu Arg Asp Gln Gln Arg Gly Gln His His *
 35 40

<11> 14
 <11> 42
 <12> PRT
 <13> Artificial Sequence

<400> 14

Glu Leu Arg Arg Arg Pro Arg Asp Arg Asp Ala Gln Leu Gln Leu Arg
 1 5 10 15
 Arg Arg Val Leu Leu Leu Gln His His Pro Ala Val Gln Gln His Leu
 20 25 30
 Glu Arg Asp Gln Gln Arg Gly Gln His His
 35 40

<210> 15
 <211> 164
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> CDS
 <222> (1)...(164)

<400> 15
 act agt ggt acc atc acc ctg ccc tgc cgc atc aag cag atc atc aac 48
 Thr Ser Gly Thr Ile Thr Leu Pro Cys Arg Ile Lys Gln Ile Ile Asn
 1 5 10 15
 atg tgg cag gag gtg ggc aag gcc atg tac gcc ccc ccc atc ggc ggc 96
 Met Trp Gln Glu Val Gly Lys Ala Met Tyr Ala Pro Pro Ile Gly Gly
 20 25 30
 cag atc aac tgc ctg agc aac atc acc gcc ctg ctg ctg acc cgc gac 144
 Gln Ile Lys Cys Leu Ser Asn Ile Thr Gly Leu Leu Leu Thr Arg Asp
 35 40 45
 ggc ggc acc gac aac tcg ag 164
 Gly Gly Ser Asp Asn Ser
 50

<210> 16
 <211> 164
 <212> PRT
 <213> Artificial Sequence

<400> 16
 Thr Ser Gly Thr Ile Thr Leu Pro Cys Arg Ile Lys Gln Ile Ile Asn
 1 5 10 15
 Met Trp Gln Glu Val Gly Lys Ala Met Tyr Ala Pro Pro Ile Gly Gly
 20 25 30
 Gln Ile Lys Cys Leu Ser Asn Ile Thr Gly Leu Leu Leu Thr Arg Asp
 35 40 45
 Gly Gly Ser Asp Asn Ser
 50

<210> 17
 <211> 200
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> CDS
 <222> (1)...(200)

<400> 17

ctc gag cag cgg caa gga gat ttt ccg ccc cgg cgg cgg cga cat gcg 48
 Leu Glu Gln Arg Gln Gly Asp Phe Pro Pro Arg Arg Arg Arg His Ala
 1 5 10 15
 cga caa ctg ggg cag cga gct gta caa gta caa ggt ggt gaa gat cga 96
 Arg Gln Leu Ala Gln Arg Ala Val Gln Val Gln Gly Gly Glu Asp Arg
 20 25 30
 gcc cct ggg cat cgc ccc cac caa ggc caa ggc ccg cgt ggt gca gcg 144
 Ala Pro Gly His Arg Pro His Gln Gly Gln Ala Pro Arg Gly Ala Ala
 35 40 45
 cga gaa ggg cgc cgt ggg cat cgg cgc tat gtc cct cgg ctt cct ggg 192
 Arg Glu Ala Arg Arg Gly His Arg Arg Tyr Val Pro Arg Leu Pro Gly
 50 55 60
 cgc tgc ag 200
 Arg Cys
 65

210: 13
 211: 65
 212: PRT
 213: Artificial Sequence

400: 18
 Leu Glu Gln Arg Gln Gly Asp Phe Pro Pro Arg Arg Arg Arg His Ala
 1 5 10 15
 Arg Gln Leu Ala Gln Arg Ala Val Gln Val Gln Gly Gly Glu Asp Arg
 20 25 30
 Ala Pro Gly His Arg Pro His Gln Gly Gln Ala Pro Arg Gly Ala Ala
 35 40 45
 Arg Glu Ala Arg Arg Gly His Arg Arg Tyr Val Pro Arg Leu Pro Gly
 50 55 60
 Arg Cys
 65

210: 19
 211: 212
 212: DNA
 213: Artificial Sequence

230:
 221: CDS
 222: (1)...(212)

400: 19
 ctc gag cag cgg caa gga gat ttt ccg ccc cgg cgg cgg cga cat gcg 48
 Leu Glu Gln Arg Gln Gly Asp Phe Pro Pro Arg Arg Arg Arg His Ala
 1 5 10 15
 cga caa ctg ggg cag cga gct gta caa gta caa ggt ggt gaa gat cga 96
 Arg Gln Leu Ala Gln Arg Ala Val Gln Val Gln Gly Gly Glu Asp Arg
 20 25 30
 gcc cct ggg cat cgc ccc cac caa ggc caa ggc ccg cgt ggt gca gcg 144
 Ala Pro Gly His Arg Pro His Gln Gly Gln Ala Pro Arg Gly Ala Ala
 35 40 45

cga gaa gag cgc cta ggg cat cgg cgc tat gtt cct cgg ctt cct ggg 192
 Arg Glu Ala Arg Leu Gly His Arg Arg Tyr Val Pro Arg Leu Pro Gly
 50 55 60

cgc tgg agc cgg ggg gat cc 212
 Arg Cys Ser Pro Gly Asp
 65 70

2100 20

2110 70

2120 PRT

2130 Artificial Sequence

2400 20

Leu Gln Gln Arg Gln Gly Asp Phe Pro Pro Arg Arg Arg Arg His Ala
 1 5 10 15
 Arg Gln Leu Ala Gln Arg Ala Val Gln Val Gln Gly Gly Glu Asp Arg
 20 25 30
 Ala Pro Gly His Arg Pro His Gln Gly Gln Ala Pro Arg Gly Ala Ala
 35 40 45
 Arg Gln Ala Arg Leu Gly His Arg Arg Tyr Val Pro Arg Leu Pro Gly
 50 55 60
 Arg Cys Ser Pro Gly Asp
 65 70

22100 21

22110 200

2220 DNA

2230 Artificial Sequence

22200

22110 CDS

22200 (1)...(200)

24000 21

ctc gaa cag cgg caa gga gat ttt cgc ccc cgg cgg cgg cga cat gcg 48
 Leu Gln Gln Arg Gln Gly Asp Phe Pro Pro Arg Arg Arg Arg His Ala
 1 5 10 15

cga caa cag gag cag cga gct gta caa gta caa ggt ggt gaa gat cga 96
 Arg Gln Leu Ala Gln Arg Ala Val Gln Val Gln Gly Gly Glu Asp Arg
 20 25 30

gcc cct gag cat cgc cct cac caa gcc caa gag cgg cgt ggt gca gcg 144
 Ala Pro Gly His Arg Pro His Gln Gly Gln Ala Pro Arg Gly Ala Ala
 35 40 45

cga gaa gag cgc cgt ggg cat cgg cgc tat gtt cct cgg ctt cct ggg 180
 Arg Gln Arg Arg Gly His Arg Arg Tyr Val Pro Arg Leu Pro Gly
 50 55 60

cgc tgg ac
 Arg Cys
 65

22100 22

<211> 66

<213> PRT

<213> Artificial Sequence

<400> 27

```

Leu Gln Gln Arg Gln Gly Asp Phe Pro Pro Arg Arg Arg Arg His Ala
 1           5           10           15
Arg Gln Leu Ala Gln Arg Ala Val Gln Val Gln Gly Gly Glu Asp Arg
 20           25           30
Ala Pro Gly His Arg Pro His Gln Gly Gln Ala Pro Arg Gly Ala Ala
 35           40           45
Arg Gln Gln Arg Arg Gly His Arg Arg Tyr Val Pro Arg Leu Pro Gly
 50           55           60
Arg Cys
65

```

<210> 25

<211> 178

<212> DNA

<213> Artificial Sequence

<220>

<221> CDS

<222> (1)...(178)

<400> 33

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ctg cag gca gca cca tgg gcg ccg cca gcc tga ccc tga ccg tgc agg      48
Leu Gln Ala Ala Pro Trp Ala Pro Pro Ala * Pro * Pro Cys Arg
 1           5           10

ccc gcc agc tgc tga gcg gca tgc tgc agc agc aga aca acc tgc tgc      96
Pro Ala Ser Cys * Ala Ala Ser Cys Ser Ser Arg Thr Thr Cys Cys
 15           20           25

gcg cca tcc agg ccc agc agc acc tgc tcc agc tga ccg tgt ggg gca      144
Ala Pro Ser Arg Pro Ser Ser Thr Cys Ser Ser * Pro Cys Gly Ala
 30           35           40

tca agc agc tcc agg ccc gcg tgc tgg ctc tag a      176
Ser Ser Ser Ser Arg Pro Ala Cys Trp Leu *
 45           50

```

<210> 24

<211> 94

<212> PRT

<213> Artificial Sequence

<400> 24

```

Leu Gln Ala Ala Pro Trp Ala Pro Pro Ala Pro Pro Cys Arg Pro Ala
 1           5           10           15
Ser Cys Ala Ala Ser Cys Ser Ser Arg Thr Thr Cys Cys Ala Pro Ser
 20           25           30
Arg Pro Ser Ser Thr Cys Ser Ser Pro Cys Gly Ala Ser Ser Ser Ser
 35           40           45
Arg Pro Ala Cys Trp Leu
50

```

<210> 25

>211> 178
 >212> DNA
 >213> Artificial Sequence

>220>
 >221> CDS
 >222> (1)...(178)

>400> 25
 ctg cag gca gca cca tgg gcg ccg cca gcc tga ccc tga ccg tgc agg 48
 Leu Glu Ala Ala Pro Trp Ala Pro Pro Ala * Pro * Pro Cys Arg
 1 5 10
 ccc gcc agc tgc tga gcg gca tgc tgc agc agc aga aca acc tgc tgc 96
 Pro Ala Ser Cys * Ala Ala Ser Cys Ser Ser Arg Thr Thr Cys Cys
 15 20 25
 gcg ccg tgc agc ccc agc agc acc tgc tcc agc tga ccg tgc ggc gca 144
 Ala Pro Ser Arg Pro Ser Ser Thr Cys Ser Ser * Pro Cys Gly Ala
 30 35 40
 tca agc agc gct ggc gcc ggc tgc tgc ctc tag a 178
 Ser Ser Ser Ala Ala Ala Ala Cys Trp Leu *
 45 50

>210> 26
 >211> 54
 >212> PRT
 >213> Artificial Sequence

>400> 26
 Leu Glu Ala Ala Pro Trp Ala Pro Pro Ala Pro Pro Cys Arg Pro Ala
 1 5 10 15
 Ser Cys Ala Ala Ser Cys Ser Ser Arg Thr Thr Cys Cys Ala Pro Ser
 20 25 30
 Arg Pro Ser Ser Thr Cys Ser Ser Pro Cys Gly Ala Ser Ser Ser Ala
 35 40 45
 Ala Ala Ala Cys Trp Leu
 50

>210> 27
 >211> 77
 >212> DNA
 >213> Artificial Sequence

>220>
 >221> CDS
 >222> (1)...(77)

>400> 27
 tct aga ggc cta cct cca gga cca ggc ctt cct ggc cat gtg ggc ctg 48
 Ser Arg Ala Leu Pro Pro Gly Pro Ala Leu Pro Gly His Val Gly Leu
 1 5 10 15
 ctc cgg caa gct gat ctg cac cac ggc cg
 Leu Arg Gln Ala Asp Leu His His Gly
 20 25

2108 28
 2110 28
 2112 PRT
 2113 Artificial Sequence

400 14
 Ser Arg Ala Leu Pro Pro Gly Pro Ala Leu Pro Gly His Val Gly Leu
 1 5 10 15
 Leu Arg Gln Ala Asp Leu His His Gly
 20 25

2109 14
 2111 140
 2112 DNA
 2113 Artificial Sequence

220
 221 CDS
 222 (1) ... (190)

400 14
 cgg cct tgg cct gga acg cca gct gga gca aca aga acc tga gcc aga 48
 Arg Pro Cys Pro Gly Thr Pro Ala Gly Ala Thr Arg Thr * Ala Arg
 1 5 10 15
 ttt gga aca aca tga cct gga tgg agt ggg agc gcg aga tca gca act 96
 Phe Gly Thr Thr * Pro Gly Trp Ser Gly Ser Ala Arg Ser Ala Thr
 20 25 30
 aca cca aga tca tct aca gcc tga tgg agg aga gcc aga acc agc agg 144
 Thr Pro Arg Ser Ser Thr Ala * Ser Arg Arg Ala Arg Thr Ser Arg
 35 40 45
 aga aga aca agc tgg acc tgc tcc agc tgg aca agt ggg caa gct t 190
 Arg Arg Thr Ser Trp Thr Cys Ser Ser Trp Thr Ser Gly Gln Ala
 50 55 60

2110 14
 2111 14
 2112 PRT
 2113 Artificial Sequence

400 30
 Arg Pro Cys Pro Gly Thr Pro Ala Gly Ala Thr Arg Thr Ala Arg Phe
 1 5 10 15
 Gly Thr Thr Pro Gly Trp Ser Gly Ser Ala Arg Ser Ala Thr Thr Pro
 20 25 30
 Arg Ser Ser Thr Ala Ser Arg Arg Ala Arg Thr Ser Arg Arg Arg Thr
 35 40 45
 Ser Trp Thr Cys Ser Ser Trp Thr Ser Gly Gln Ala
 50 55 60

2110 14
 2111 177
 2112 DNA
 2113 Artificial Sequence

<220>

<221> CDS

<222> (1)...(177)

<400> 31

aag	ctt	gtg	gaa	ctg	gtt	caa	cat	cac	caa	ctg	gct	gtg	gta	cat	caa	48
Lys	Leu	Val	Glu	Leu	Val	Gln	His	His	Gln	Leu	Ala	Val	Val	His	Gln	
1			5						10					15		

gat	ttt	cat	cat	gat	cgt	ggg	cgg	cct	gat	cgg	cct	gcg	cat	cgt	gtt	96
Asp	Phe	His	His	Asp	Arg	Gly	Arg	Pro	Asp	Arg	Pro	Ala	His	Arg	Val	
			20					25					30			

caa	cgt	ggt	gag	cat	cgt	gaa	cgg	cgt	gcg	cca	ggg	cta	cag	ccc	cct	144
His	Arg	Ala	Glu	His	Arg	Glu	Pro	Arg	Ala	Pro	Gly	Leu	Gln	Pro	Pro	
		35				40						45				

gag	ctt	caa	gac	cgg	cct	gcc	cgt	gcc	cgg	cgg						177
Glu	Leu	Pro	Asp	Pro	Pro	Ala	Arg	Ala	Pro	Arg						
	50						55									

<210> 31

<211> 59

<212> PRT

<213> Artificial Sequence

<400> 31

Lys	Leu	Val	Glu	Leu	Val	Gln	His	His	Gln	Leu	Ala	Val	Val	His	Gln	
1			5						10					15		
Asp	Phe	His	His	Asp	Arg	Gly	Arg	Pro	Asp	Arg	Pro	Ala	His	Arg	Val	
			20					25					30			
His	Arg	Ala	Glu	His	Arg	Glu	Pro	Arg	Ala	Pro	Gly	Leu	Gln	Pro	Pro	
		35				40						45				
Glu	Leu	Pro	Asp	Pro	Pro	Ala	Arg	Ala	Pro	Arg						
	50						55									

<210> 33

<211> 140

<212> DNA

<213> Artificial Sequence

<220>

<221> CDS

<222> (1)...(140)

<400> 33

cgg	cgg	ccc	cga	cgg	ccc	cga	ggg	cat	cga	gga	gga	ggg	cgg	cga	ggg	48
Pro	Arg	Pro	Arg	Pro	Pro	Arg	Gly	His	Arg	Gly	Gly	Gly	Arg	Arg	Ala	
1			5						10					15		

cga	ccg	cga	cag	cag	cac	cgg	cct	ggt	gac	cgg	ctt	cct	gcc	cct	gat	96
Arg	Pro	Arg	Pro	Gln	His	Pro	Pro	Gly	Asp	Arg	Leu	Pro	Ala	Pro	Asp	
			20					25					30			

ctg	gga	caa	cct	ggg	cag	cct	gtt	cct	gtt	cag	cta	cca	tgg	at		144
Leu	Gly	Arg	Pro	Ala	Gln	Pro	Val	Pro	Val	Gln	Leu	Pro	Ser			
		35					40					45				

<210> 34
 <211> 46
 <212> PRT
 <213> Artificial Sequence

<400> 34
 Pro Arg Pro Arg Pro Pro Arg Gly His Arg Gly Gly Gly Arg Arg Ala
 1 5 10 15
 Arg Pro Arg Pro Gln His Pro Pro Gly Asp Arg Leu Pro Ala Pro Asp
 20 25 30
 Leu Gly Arg Pro Ala Gln Pro Val Pro Val Gln Leu Pro Ser
 35 40 45

<210> 35
 <211> 129
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> CDS
 <222> (1)...(129)

<400> 35
 atc gat tgc gcg acc tgc tgc tga tgc tgg ccc gca tgc tgg agc tgc 48
 Ile Asp Cys Ala Thr Cys Cys * Ser Trp Pro Ala Ser Trp Ser Cys
 1 5 10 15
 tgg gcc ggc gcg gct ggg aga tcc tga agt act ggt gga acc tgc tcc 96
 Trp Ala Gly Ala Ala Gly Arg Ser * Ser Thr Gly Gly Thr Cys Ser
 20 25 30
 agt act gga gcc agg agc tga aga act ctg cag 129
 Ser Thr Gly Ala Arg Ser * Arg Thr Leu Gln
 35 40

<210> 36
 <211> 40
 <212> PPT
 <213> Artificial Sequence

<400> 36
 Ile Asp Cys Ala Thr Cys Cys Ser Trp Pro Ala Ser Trp Ser Cys Trp
 1 5 10 15
 Ala Gly Ala Ala Gly Arg Ser Ser Thr Gly Gly Thr Cys Ser Ser Thr
 20 25 30
 Gly Ala Arg Ser Arg Thr Leu Gln
 35 40

<210> 37
 <211> 114
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> CDS
 <222> (1)...(114)

<400> 37
 ctg cag tga gcc tgc tga aag cca cag cca tgg cag agg gca 48
 Leu Gln * Ala Cys * Thr Pro Pro Pro Ser Pro Trp Pro Arg Ala
 1 5 10
 ccg acc gag tga tgg agg tgg tgc agc gca tct ggc gag gca tcc tgc 96
 Pro Thr Ala * Ser Arg Trp Cys Ser Ala Ser Gly Ala Ala Ser Cys
 15 20 25
 aca tct cca ccc gaa ttc 114
 Thr Ser Pro Pro Glu Phe
 30 35

210 * 38
 211 * 35
 212 * FRT
 213 * Artificial Sequence

<400> 38
 Leu Gln Ala Cys Thr Pro Pro Pro Ser Pro Trp Pro Arg Ala Pro Thr
 1 5 10 15
 Ala Ser Arg Trp Cys Ser Ala Ser Gly Ala Ala Ser Cys Thr Ser Pro
 20 25 30
 Pro Glu Phe
 35

210 * 39
 211 * 41
 212 * DNA
 213 * Artificial Sequence

220 *
 221 * CDS
 222 * (1)...(41)

<400> 39
 gaa ttt gct agg gct tgg agc gcg ccc tgc tgt aag gat cc 41
 Glu Phe Ala Arg Ala Ser Ser Ala Pro Cys Cys Lys Asp
 1 5 10

210 * 40
 211 * 13
 212 * FRT
 213 * Artificial Sequence

<400> 40
 Glu Phe Ala Arg Ala Ser Ser Ala Pro Cys Cys Lys Asp
 1 5 10

210 * 41
 211 * 506
 212 * DNA
 213 * Artificial Sequence

220 *
 221 * CDS
 222 * (1)...(506)

<400> 41
 ggt agt ggt gcc gac cgc ctg tgg gtg acc gtg tac tac gcc gtg ccc 48
 Ala Ser Ala Ala Asp Arg Leu Trp Val Thr Val Tyr Tyr Gly Val Pro
 1 5 10 15
 gtg tgg aag gac gcc acc acc acc ctg ttc tgc gcc agc gac gcc aag 96
 Val Trp Lys Asp Ala Thr Thr Thr Leu Phe Cys Ala Ser Asp Ala Lys
 20 25 30
 gcc tac gac acc gag gtg cac aac gtg tgg gcc acc cac gcc tgc gtg 144
 Ala Tyr Asp Thr Glu Val His Asn Val Trp Ala Thr His Ala Cys Val
 35 40 45
 ccc acc gac ccc aac ccc cag gag gtg gtg ctg gcc aac gtg acc gag 192
 Pro Thr Asp Pro Asn Pro Gln Glu Val Val Leu Gly Asn Val Thr Glu
 50 55 60
 aac ttc aac atg gcc aag aac aac atg gtg gag cag atg cac gag gat 240
 Asn Phe Asn Met Gly Lys Asn Asn Met Val Glu Gln Met His Glu Asp
 65 70 75 80
 atc atc acc ctg tgg gac cag agc ctg aag ccc tgc gtg aag ctg acc 288
 Ile Ile Ser Leu Trp Asp Gln Ser Leu Lys Pro Cys Val Lys Leu Thr
 85 90 95
 ccc ctg tgc gtg acc ctg aac tgc acc aag ctg aag aac agc acc gac 336
 Pro Leu Cys Val Thr Leu Asn Cys Thr Lys Leu Lys Asn Ser Thr Asp
 100 105 110
 acc aac aac acc cgc tgg gcc acc cag gag atg aag aac tgc agc ttc 384
 Thr Asn Asn Thr Arg Trp Gly Thr Gln Glu Met Lys Asn Cys Ser Phe
 115 120 125
 aac atc acc acc agc gtg tgc aac aag atg aag cgc gag tac gcc ctg 432
 Asn Ile Ser Thr Ser Val Arg Asn Lys Met Lys Arg Glu Tyr Ala Leu
 130 135 140
 ttc tac acc ctg gac atc gtg ccc atc gac aac gag aac acc agc tac 480
 Phe Tyr Ser Leu Asp Ile Val Pro Ile Asp Asn Asp Asn Thr Ser Tyr
 145 150 155 160
 cgc ctg cgc agc tgc aac aca tgc at 506
 Arg Leu Arg Ser Cys Asn Thr Ser
 165

<210> 42

<211> 168

<212> PRT

<213> Artificial Sequence

<400> 42
 Ala Ser Ala Ala Asp Arg Leu Trp Val Thr Val Tyr Tyr Gly Val Pro
 1 5 10 15
 Val Trp Lys Asp Ala Thr Thr Thr Leu Phe Cys Ala Ser Asp Ala Lys
 20 25 30
 Ala Tyr Asp Thr Glu Val His Asn Val Trp Ala Thr His Ala Cys Val
 35 40 45

Pro Thr Asp Pro Asn Pro Gln Glu Val Val Leu Gly Asn Val Thr Glu
 50 55 60
 Asn Phe Asn Met Gly Lys Asn Asn Met Val Glu Gln Met His Glu Asp
 65 70 75 80
 Ile Ile Ser Leu Trp Asp Gln Ser Leu Lys Pro Cys Val Lys Leu Thr
 85 90 95
 Pro Leu Cys Val Thr Leu Asn Cys Thr Lys Leu Lys Asn Ser Thr Asp
 100 105 110
 Thr Asn Asn Thr Arg Trp Gly Thr Gln Glu Met Lys Asn Cys Ser Phe
 115 120 125
 Asn Ile Ser Thr Ser Val Arg Asn Lys Met Lys Arg Glu Tyr Ala Leu
 130 135 140
 Phe Tyr Ser Leu Asp Ile Val Pro Ile Asp Asn Asp Asn Thr Ser Tyr
 145 150 155 160
 Arg Leu Arg Ser Cys Asn Thr Ser
 165

<210> 43
 <211> 374
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> CDS
 <222> (1)...(374)

<400> 43

tct aga acc aac tgg acc aac acc ctg aag cgc gtg gcc gag aag ctg 48
 Ser Arg Thr Asn Trp Thr Asn Thr Leu Lys Arg Val Ala Glu Lys Leu
 1 5 10 15
 cgc gag aag ttc aac aac acc acc atc gtg ttc aac cag agc tcc ggc 96
 Arg Glu Lys Phe Asn Asn Thr Thr Ile Val Phe Asn Gln Ser Ser Gly
 20 25 30
 ggc gac ccc gag atc gtg atg cac agc ttc aac tgc ggc ggc gag ttc 144
 Gly Asp Pro Glu Ile Val Met His Ser Phe Asn Cys Gly Gly Glu Phe
 35 40 45
 ttc tac tgc aac acc acc cag ctg ttc aac agc acc tgg aac gag acc 192
 Phe Tyr Cys Asn Thr Thr Gln Leu Phe Asn Ser Thr Trp Asn Glu Thr
 50 55 60
 aac agc gag ggc aac atc act agt ggc acc atc acc ctg ccc tgc cgc 240
 Asn Ser Glu Gly Asn Ile Thr Ser Gly Thr Ile Thr Leu Pro Cys Arg
 65 70 75 80
 atc aag cag atc atc aac atg tgg cag gag gtg ggc aag gcc atg tac 288
 Ile Lys Gln Ile Ile Asn Met Trp Gln Glu Val Gly Lys Ala Met Tyr
 85 90 95
 gcc ccc ccc atc ggc ggc cag atc aag tgc ctg agc aac atc acc ggc 336
 Ala Pro Pro Ile Gly Gly Gln Ile Lys Cys Leu Ser Asn Ile Thr Gly
 100 105 110
 ctg ctg ctg acc cgc gac ggc ggc agc gac aac tgc ag 374
 Leu Leu Leu Thr Arg Asp Gly Gly Ser Asp Asn Ser
 115 120

-210- 44
 -211- 124
 -212- PRT
 -213- Artificial Sequence

-400- 41
 Ser Arg Thr Asn Trp Thr Asn Thr Leu Lys Arg Val Ala Glu Lys Leu
 1 5 10 15
 Arg Gln Lys Phe Asn Asn Thr Thr Ile Val Phe Asn Gln Ser Ser Gly
 20 25 30
 Gly Asp Pro Glu Ile Val Met His Ser Phe Asn Cys Gly Gly Glu Phe
 35 40 45
 Phe Tyr Cys Asn Thr Thr Gln Leu Phe Asn Ser Thr Trp Asn Glu Thr
 50 55 60
 Asn Ser Glu Gly Asn Ile Thr Ser Gly Thr Ile Thr Leu Pro Cys Arg
 65 70 75 80
 Ile Lys Gln Ile Ile Asn Met Trp Gln Glu Val Gly Lys Ala Met Tyr
 85 90 95
 Ala Pro Pro Ile Gly Gly Gln Ile Lys Cys Leu Ser Asn Ile Thr Gly
 100 105 110
 Leu Leu Leu Thr Arg Asp Gly Gly Ser Asp Asn Ser
 115 120

-210- 45
 -211- 1277
 -212- DNA
 -213- Artificial Sequence

-220-
 -221- CDS
 -222- (1)...(1277)

-400- 45
 gcc agc ggc gcc gac cgc ctg tgg gtg acc gtg tac tac gcc gtg ccc 48
 Ala Ser Ala Ala Asp Arg Leu Trp Val Thr Val Tyr Tyr Gly Val Pro
 1 5 10 15
 gtg tgu aag gac gcc acc acc acc ctg ttc tgc gcc agc gac gcc aag 96
 Val Trp Lys Asp Ala Thr Thr Thr Leu Phe Cys Ala Ser Asp Ala Lys
 20 25 30
 gcc tac gac acc gag gtg cac aac gtg tgg gcc acc cac gcc tgc gtg 144
 Ala Tyr Asp Thr Glu Val His Asn Val Trp Ala Thr His Ala Cys Val
 35 40 45
 ccc acc gac ccc aac ccc cag gag gtg gtg ctg gcc aac gtg acc gag 192
 Pro Thr Asp Pro Asn Pro Gln Glu Val Val Leu Gly Asn Val Thr Glu
 50 55 60
 aac ttc aac atg gcc aag aac aac atg gtg gag cag atg cac gag gat 240
 Asn Phe Asn Met Gly Lys Asn Asn Met Val Glu Gln Met His Glu Asp
 65 70 75 80
 atc atc agc ctg tgg gac cag agc ctg aag ccc tgc gtg aag ctg acc
 Ile Ile Ser Leu Trp Asp Gln Ser Leu Lys Pro Cys Val Lys Leu Thr
 85 90 95
 ccc ctg tgc gtg acc ctg aac tgc acc aag ctg aag aac agc acc gac

Pro	Leu	Cys	Val	Thr	Leu	Asn	Cys	Thr	Lys	Leu	Lys	Asn	Ser	Thr	Asp	
			100					105					110			
acc	aac	aac	acc	ggc	tgg	ggc	acc	cag	gag	atg	aag	aac	tgc	agc	ttc	384
Thr	Asn	Asn	Thr	Arg	Trp	Gly	Thr	Gln	Glu	Met	Lys	Asn	Cys	Ser	Phe	
			115				120					125				
aac	atc	agc	acc	agc	gtg	ggc	aac	aag	atg	aag	ggc	gag	tac	gcc	ctg	432
Asn	Ile	Ser	Thr	Ser	Val	Arg	Asn	Lys	Met	Lys	Arg	Glu	Tyr	Ala	Leu	
			130				135					140				
ttc	tac	agc	ctg	gac	atc	gtg	ccc	atc	gac	aac	gac	aac	acc	agc	tac	480
Phe	Tyr	Ser	Leu	Asp	Ile	Val	Pro	Ile	Asp	Asn	Asp	Asn	Thr	Ser	Tyr	
			145			150				155					160	
ggc	ctg	ggc	agg	tgc	aac	aca	tgg	atc	atc	acc	cag	ggc	tgc	ccc	aag	528
Arg	Leu	Arg	Ser	Cys	Asn	Thr	Ser	Ile	Ile	Thr	Gln	Ala	Cys	Pro	Lys	
				165						170				175		
gtg	agc	ttc	gag	ccc	atc	ccc	atc	cac	ttc	tgc	ggc	ccc	ggc	ggc	ttc	576
Val	Ser	Phe	Glu	Pro	Ile	Pro	Ile	His	Phe	Cys	Ala	Pro	Ala	Gly	Phe	
			180					185					190			
ggc	atc	ctg	aag	tgc	aac	aac	aag	acc	ttc	aac	ggc	acc	ggc	ccc	tgc	624
Ala	Ile	Leu	Lys	Cys	Asn	Asn	Lys	Thr	Phe	Asn	Gly	Thr	Gly	Pro	Cys	
			195				200					205				
acc	aac	gtg	agg	acc	gtg	cag	tgc	acc	cac	gga	att	ggc	ccc	gtg	gtg	672
Thr	Asn	Val	Ser	Thr	Val	Gln	Cys	Thr	His	Gly	Ile	Arg	Pro	Val	Val	
			210				215					220				
agc	acc	cag	ctg	ctg	ctg	aac	ggc	agg	ctg	ggc	gag	gag	gag	gtg	gtg	720
Ser	Thr	Gln	Leu	Leu	Leu	Asn	Gly	Ser	Leu	Ala	Glu	Glu	Glu	Val	Val	
			225			230				235				240		
atc	aga	tct	gag	aac	ttc	acc	aac	aac	ggc	aag	acc	atc	atc	gtg	cag	768
Ile	Arg	Ser	Glu	Asn	Phe	Thr	Asn	Asn	Ala	Lys	Thr	Ile	Ile	Val	Gln	
				245					250					255		
ctg	aac	gag	agg	gtg	gag	atc	aac	tgc	acc	ggc	ccc	aac	aac	aac	acc	816
Leu	Asn	Glu	Ser	Val	Glu	Ile	Asn	Cys	Thr	Arg	Pro	Asn	Asn	Asn	Thr	
			260					265					270			
ggc	aag	agg	atc	cac	atc	ggc	ccc	ggc	ggc	ggc	ttc	tac	acc	acc	ggc	864
Arg	Lys	Ser	Ile	His	Ile	Gly	Pro	Gly	Arg	Ala	Phe	Tyr	Thr	Thr	Gly	
			275				280					285				
gac	atc	atc	ggc	gac	atc	ggc	cag	ggc	cac	tgc	aac	atc	tct	aga	acc	912
Asp	Ile	Ile	Gly	Asp	Ile	Arg	Gln	Ala	His	Cys	Asn	Ile	Ser	Arg	Thr	
			290			295					300					
aac	tgg	acc	aac	acc	ctg	aag	ggc	gtg	ggc	gag	aag	ctg	ggc	gag	aag	960
Asn	Trp	Thr	Asn	Thr	Leu	Lys	Arg	Val	Ala	Glu	Lys	Leu	Arg	Glu	Lys	
			305			310				315				320		
ttc	aac	aac	acc	acc	atc	gtg	ttc	aac	cag	agg	tct	ggc	ggc	gac	ccc	
Phe	Asn	Asn	Thr	Thr	Ile	Val	Phe	Asn	Gln	Ser	Ser	Gly	Gly	Asp	Pro	
			325					330						335		

gag atc ggg atg cac agc ttc aac tgc ggc ggc gag ttc ttc tac tgc 1056
 Glu Ile Val Met His Ser Phe Asn Cys Gly Gly Glu Phe Phe Tyr Cys
 340 345 350
 aac acc acc cag ctg ttc aac agc acc tgg aac gag acc aac agc gag 1104
 Asn Thr Thr Gln Leu Phe Asn Ser Thr Trp Asn Glu Thr Asn Ser Glu
 355 360 365
 ggc aac atc act agt ggc acc atc acc ctg ccc tgc tgc atc aag cag 1152
 Gly Asn Ile Thr Ser Gly Thr Ile Thr Leu Pro Cys Arg Ile Lys Gln
 370 375 380
~~atc~~ atc aac atg tgg cag gag gtg ggc aag ggc atg tac gcc ccc ccc 1200
 Ile Ile Asn Met Trp Gln Glu Val Gly Lys Ala Met Tyr Ala Pro Pro
 385 390 395 400
 atc ggc ggc cag atc aag tgc ctg agc aac atc acc ggc ctg ctg ctg 1248
 Ile Gly Gly Gln Ile Lys Cys Leu Ser Asn Ile Thr Gly Leu Leu Leu
 405 410 415
 acc cgc gac ggc ggc agc gac aac tgc ag 1272
 Thr Arg Asp Gly Gly Ser Asp Asn Ser
 420 425

<210> 46

<211> 425

<212> PRT

<213> Artificial Sequence

<400> 46

Ala Ser Ala Ala Asp Arg Leu Trp Val Thr Val Tyr Tyr Gly Val Pro
 1 5 10 15
 Val Trp Lys Asp Ala Thr Thr Thr Leu Phe Cys Ala Ser Asp Ala Lys
 20 25 30
 Ala Tyr Asp Thr Glu Val His Asn Val Trp Ala Thr His Ala Cys Val
 35 40 45
 Pro Thr Asp Pro Asn Pro Gln Glu Val Val Leu Gly Asn Val Thr Glu
 50 55 60
 Asn Phe Asn Met Gly Lys Asn Asn Met Val Glu Gln Met His Glu Asp
 65 70 75 80
 Ile Ile Ser Leu Trp Asp Gln Ser Leu Lys Pro Cys Val Lys Leu Thr
 85 90 95
 Pro Leu Cys Val Thr Leu Asn Cys Thr Lys Leu Lys Asn Ser Thr Asp
 100 105 110
 Thr Asn Asn Thr Arg Trp Gly Thr Gln Glu Met Lys Asn Cys Ser Phe
 115 120 125
 Asn Ile Ser Thr Ser Val Arg Asn Lys Met Lys Arg Glu Tyr Ala Leu
 130 135 140
 Phe Tyr Ser Leu Asp Ile Val Pro Ile Asp Asn Asp Asn Thr Ser Tyr
 145 150 155 160
 Arg Leu Arg Ser Cys Asn Thr Ser Ile Ile Thr Gln Ala Cys Pro Lys
 165 170 175
 Val Ser Phe Glu Pro Ile Pro Ile His Phe Cys Ala Pro Ala Gly Phe
 180 185 190
 Ala Ile Leu Lys Cys Asn Asn Lys Thr Phe Asn Gly Thr Gly Pro Cys
 195 200 205
 Thr Asn Val Ser Thr Val Gln Cys Thr His Gly Ile Arg Pro Val Val
 210 215 220

Ser Thr Gln Leu Leu Leu Asn Gly Ser Leu Ala Glu Glu Glu Val Val
 225 230 235 240
 Ile Arg Ser Glu Asn Phe Thr Asn Asn Ala Lys Thr Ile Ile Val Gln
 245 250 255
 Leu Asn Glu Ser Val Glu Ile Asn Cys Thr Arg Pro Asn Asn Asn Thr
 260 265 270
 Arg Lys Ser Ile His Ile Gly Pro Gly Arg Ala Phe Tyr Thr Thr Gly
 275 280 285
 Asp Ile Ile Gly Asp Ile Arg Gln Ala His Cys Asn Ile Ser Arg Thr
 290 295 300
 Asn Trp Thr Asn Thr Leu Lys Arg Val Ala Glu Lys Leu Arg Glu Lys
 305 310 315 320
 Phe Asn Asn Thr Thr Ile Val Phe Asn Gln Ser Ser Gly Gly Asp Pro
 325 330 335
 Glu Ile Val Met His Ser Phe Asn Cys Gly Gly Glu Phe Phe Tyr Cys
 340 345 350
 Asn Thr Thr Gln Leu Phe Asn Ser Thr Trp Asn Glu Thr Asn Ser Glu
 355 360 365
 Gly Asn Ile Thr Ser Gly Thr Ile Thr Leu Pro Cys Arg Ile Lys Gln
 370 375 380
 Ile Ile Asn Met Trp Gln Glu Val Gly Lys Ala Met Tyr Ala Pro Pro
 385 390 395 400
 Ile Gly Gly Gln Ile Lys Cys Leu Ser Asn Ile Thr Gly Leu Leu Leu
 405 410 415
 Thr Arg Asp Gly Ser Asp Asn Ser
 420 425

(211) 47

(211) 1277

(213) DNA

(213) Artificial Sequence

(220)

(221) CDS

(221) (1)...(1277)

(400) 47

gct agt ggt gac gac cgc ctg tgg gtg acc gtg tac tac gcc gtg ccc 48
 Ala Ser Ala Ala Asp Arg Leu Trp Val Thr Val Tyr Tyr Gly Val Pro
 1 5 10 15
 gtg tgg aag gac gcc acc acc acc ctg ttc tgc gcc agc gac gcc aag 96
 Val Trp Lys Asp Ala Thr Thr Thr Leu Phe Cys Ala Ser Asp Ala Lys
 20 25 30
 gcc tac gac acc gag gtg cac aac gtg tgg gcc acc cac gcg tgc gtg 144
 Ala Tyr Asp Thr Glu Val His Asn Val Trp Ala Thr His Ala Cys Val
 35 40 45
 ccc acc gac ccc aac ccc cag gag gtg gtg ctg gcc aac gtg acc gag 192
 Pro Thr Asp Pro Asn Pro Gln Glu Val Val Leu Gly Asn Val Thr Glu
 50 55 60
 aac ttc aac atg gcc aag aac aac atc gtg gag cag atg cac gag gat 240
 Asn Phe Asn Met Gly Lys Asn Asn Met Val Glu Gln Met His Glu Asp
 65 70 75 80
 atc atc agc ctg tgg gac cag agc ctg aag ccc tgc gtg aag ctg acc 296
 Ile Ile Ser Leu Trp Asp Gln Ser Leu Lys Pro Cys Val Lys Leu Thr

85								90				95				
ccc	ctg	tgc	gtg	acc	ctg	caa	tgc	acc	aag	ctg	aag	cag	agg	acc	gac	336
Pro	Leu	Cys	Val	Thr	Leu	Gln	Cys	Thr	Lys	Leu	Lys	Gln	Ser	Thr	Asp	
			100					105					110			
acc	cag	aac	acc	ggc	tgg	ggc	acc	cag	gag	atg	aag	aac	tgc	agg	ttc	384
Thr	Gln	Asn	Thr	Arg	Trp	Gly	Thr	Gln	Glu	Met	Lys	Asn	Cys	Ser	Phe	
		115					120					125				
aac	atc	agg	acc	agg	gtg	ggc	aac	aag	atg	aag	ggc	gag	tac	ggc	ctg	432
Asn	Ile	Ser	Thr	Ser	Val	Arg	Asn	Lys	Met	Lys	Arg	Glu	Tyr	Ala	Leu	
	130					135						140				
ttc	tac	agg	ctg	gac	atc	gtg	ccc	atc	gac	aac	gac	aac	acc	agg	tac	480
Phe	Tyr	Ser	Leu	Asp	Ile	Val	Pro	Ile	Asp	Asn	Asp	Asn	Thr	Ser	Tyr	
	145				150					155					160	
ggc	ctg	ggc	agg	tgc	aac	aca	tgg	atc	atc	acc	cag	ggc	tgc	ccc	aag	528
Arg	Leu	Arg	Ser	Lys	Asn	Thr	Ser	Ile	Ile	Thr	Gln	Ala	Cys	Pro	Lys	
			165					170						175		
gtg	agg	ttc	gag	ccc	atc	ccc	atc	ccc	ttc	tgc	ggc	ccc	ggc	ggc	ttc	576
Val	Ser	Phe	Glu	Pro	Ile	Pro	Ile	His	Phe	Cys	Ala	Pro	Ala	Gly	Phe	
			180					185					190			
ggc	atc	ctg	aag	tgc	aac	aac	aag	acc	ttc	aac	ggc	acc	ggc	ccc	tgc	624
Ala	Ile	Leu	Lys	Cys	Asn	Asn	Lys	Thr	Phe	Asn	Gly	Thr	Gly	Pro	Cys	
		195					200					205				
acc	aac	gtg	agg	acc	gtg	cag	tgc	acc	cac	gga	att	ggc	ccc	gtg	gtg	672
Thr	Asn	Val	Ser	Thr	Val	Gln	Cys	Thr	His	Gly	Ile	Arg	Pro	Val	Val	
	210					215					220					
agg	acc	cag	ctg	ctg	ctg	aac	ggc	agg	ctg	ggc	gag	gag	gag	gtg	gtg	720
Ser	Thr	Gln	Leu	Leu		Asn	Gly	Ser	Leu	Ala	Glu	Glu	Glu	Val	Val	
	225				230					235				240		
atc	aga	tct	gag	aac	ttc	acc	aac	aac	ggc	aag	acc	atc	atc	gtg	cag	768
Ile	Arg	Ser	Glu	Asn	Phe	Thr	Asn	Asn	Ala	Lys	Thr	Ile	Ile	Val	Gln	
			245						250					255		
ctg	aac	gag	agg	gtg	gag	atc	aac	tgc	acc	ggc	ccc	aac	aac	aac	acc	816
Leu	Asn	Glu	Ser	Val	Glu	Ile	Asn	Cys	Thr	Arg	Pro	Asn	Asn	Asn	Thr	
			260					265					270			
ggc	aag	agg	atc	ccc	atc	ggc	ccc	ggc	ggc	ggc	ttc	tac	acc	acc	ggc	864
Arg	Lys	Ser	Ile	His	Ile	Gly	Pro	Gly	Arg	Ala	Phe	Tyr	Thr	Thr	Gly	
		275					280					285				
gac	atc	atc	ggc	gac	atc	ggc	cag	ggc	cac	tgc	aac	atc	tct	aga	acc	912
Asp	Ile	Ile	Gly	Asp	Ile	Arg	Gln	Ala	His	Cys	Asn	Ile	Ser	Arg	Thr	
	290					295					300					
aac	tgg	acc	aac	acc	ctg	aag	ggc	gtg	ggc	gag	aag	ctg	ggc	gag	aag	
Asn	Trp	Thr	Asn	Thr	Leu	Lys	Arg	Val	Ala	Glu	Lys	Leu	Arg	Glu	Lys	
	305				310					315				320		
ttc	aac	aac	acc	acc	atc	gtg	ttc	aac	cag	agg	tcc	ggc	ggc	gag	ccc	

Phe Asn Asn Thr Thr Ile Val Phe Asn Gln Ser Ser Gly Gly Asp Pro
 325 330 335
 gag atc gtg atg cac agc ttc aac tgc ggc ggc gag ttc ttc tac tgc 1056
 Glu Ile Val Met His Ser Phe Asn Cys Gly Gly Glu Phe Phe Tyr Cys
 340 345 350
 aac acc acc cag ctg ttc aac agc acc tgg aac gag acc aac agc gag 1104
 Asn Thr Thr Gln Leu Phe Asn Ser Thr Trp Asn Glu Thr Asn Ser Glu
 355 360 365
 ggc aac atc act agt ggc acc atc acc ctg acc tgc cgc atc aag cag 1152
 Gly Asn Ile Thr Ser Gly Thr Ile Thr Leu Pro Cys Arg Ile Lys Gln
 370 375 380
 atc atc aac atg tgg cag gag gtg ggc aag ggc atg tac gcc ccc ccc 1200
 Ile Ile Asn Met Trp Gln Glu Val Gly Lys Ala Met Tyr Ala Pro Pro
 385 390 395 400
 atc ggc ggc cag atc aag tgc ctg agc aac atc acc ggc ctg ctg ctg 1248
 Ile Gly Gly Gln Ile Lys Cys Leu Ser Asn Ile Thr Gly Leu Leu Leu
 405 410 415
 acc cgc gac ggc ggc agc gac aac tgc ag 1277
 Thr Arg Asp Gly Gly Ser Asp Asn Ser
 420 425

*2100 48
 *2110 425
 *2120 PRT
 *2130 Artificial Sequence

*4000 48
 Ala Ser Ala Ala Asp Arg Leu Trp Val Thr Val Tyr Tyr Gly Val Pro
 1 5 10 15
 Val Trp Lys Asp Ala Thr Thr Thr Leu Phe Cys Ala Ser Asp Ala Lys
 20 25 30
 Ala Tyr Asp Thr Glu Val His Asn Val Trp Ala Thr His Ala Cys Val
 35 40 45
 Pro Thr Asp Pro Asn Pro Gln Glu Val Val Leu Gly Asn Val Thr Glu
 50 55 60
 Asn Phe Asn Met Gly Lys Asn Asn Met Val Glu Gln Met His Glu Asp
 65 70 75 80
 Ile Ile Ser Leu Trp Asp Gln Ser Leu Lys Pro Cys Val Lys Leu Thr
 85 90 95
 Pro Leu Cys Val Thr Leu Gln Cys Thr Lys Leu Lys Gln Ser Thr Asp
 100 105 110
 Thr Gln Asn Thr Arg Trp Gly Thr Gln Glu Met Lys Asn Cys Ser Phe
 115 120 125
 Asn Ile Ser Thr Ser Val Arg Asn Lys Met Lys Arg Glu Tyr Ala Leu
 130 135 140
 Phe Tyr Ser Leu Asp Ile Val Pro Ile Asp Asn Asp Asn Thr Ser Tyr
 145 150 155 160
 Arg Leu Arg Ser Cys Asn Thr Ser Ile Ile Thr Gln Ala Cys Pro Lys
 165 170 175
 Val Ser Phe Glu Pro Ile Pro Ile His Phe Cys Ala Pro Ala Gly Phe
 180 185 190
 Ala Ile Leu Lys Cys Asn Asn Lys Thr Phe Asn Gly Thr Gly Pro Cys

195	200	205
Thr Asn Val Ser Thr Val Gln Cys Thr His Gly Ile Arg Pro Val Val		
210	215	220
Ser Thr Gln Leu Leu Leu Asn Gly Ser Leu Ala Glu Glu Glu Val Val		
225	230	235
Ile Arg Ser Glu Asn Phe Thr Asn Asn Ala Lys Thr Ile Ile Val Gln		
245	250	255
Leu Asn Glu Ser Val Glu Ile Asn Cys Thr Arg Pro Asn Asn Asn Thr		
260	265	270
Arg Lys Ser Ile His Ile Gly Pro Gly Arg Ala Phe Tyr Thr Thr Gly		
275	280	285
Asp Ile Ile Gly Asp Ile Arg Gln Ala His Cys Asn Ile Ser Arg Thr		
290	295	300
Asn Trp Thr Asn Thr Leu Lys Arg Val Ala Glu Lys Leu Arg Glu Lys		
305	310	315
Phe Asn Asn Thr Thr Ile Val Phe Asn Gln Ser Ser Gly Gly Asp Pro		
325	330	335
Glu Ile Val Met His Ser Phe Asn Cys Gly Gly Glu Phe Phe Tyr Cys		
340	345	350
Asn Thr Thr Gln Leu Phe Asn Ser Thr Trp Asn Glu Thr Asn Ser Glu		
355	360	365
Gly Asn Ile Thr Ser Gly Thr Ile Thr Leu Pro Cys Arg Ile Lys Gln		
370	375	380
Ile Ile Asn Met Trp Gln Glu Val Gly Lys Ala Met Tyr Ala Pro Pro		
385	390	395
Ile Gly Gly Gln Ile Lys Cys Leu Ser Asn Ile Thr Gly Leu Leu Leu		
405	410	415
Thr Arg Asp Gly Gly Ser Asp Asn Ser		
420	425	

<210> 49

<211> 144

<212> PRT

<213> Artificial Sequence

<400> 49

gct agt ggg ggc gac cgc ctg tgg gtg acc gtg tac tac ggc gtg acc	48
gtg tgg aag gac ggc acc acc acc ctg ttc tgc gcc agc gac gcc aag	96
gcc tac gac acc gag gtg cac aac tgg tgg gcc acc cac ggc tgc gtg	144
ccc acc gac ccc aac ccc cag gag gtg gtg ctg ggc aac gtg acc gag	192
aac ttc aac atg ggc aag aac aac atg gtg gag cag atg cac gag gat	240
atc atc agc ctg tgg gac cag agc ctg aag ccc tgc gtg aag ctg acc	288
ccc ctg tgc gtg acc ctg caa tgc acc aag ctg aag cag agc acc gac	336
acc cag aac acc cgc tgg ggc acc cag gag atg aag aac tgc agc ttc	384
cag atc agc acc agc gtg cgc aac aag atg aag cgc gag tac gcc ctg	432
ttc tac agc ctg gac atc gtg ccc atc gac aac gac cag acc agc tac	480
cgc ctg cgc agc tgc aac aca tgc atc atc acc cag gcc tgc ccc aag	528
gtg agc ttc gag ccc atc ccc atc cac ttc tgc gcc ccc gcc ggc ttc	576
gcc atc ctg aag tgc aac aac aag acc ttc aac ggc acc gcc ccc tgc	624
acc aac ctg agc acc gtg cag tgc acc cac gga att cgc ccc gtg gtg	672
agc acc cag ctg ctg ctg aac ggc agc ctg gcc gag gag gag gtg gtg	720
atc aga ttc aag aac ttc acc aac aac gcc aag acc atc atc gtg cag	768
ctg aac gag agc gtg gag atc aac tgc acc cgc ccc aac aac aac acc	816
cgc aag agc atc cac atc ggc ccc ggc gcc ttc tac acc acc gcc	864
gac atc atc ggc gac atc cgc cag gcc cac tgc aac atc tct aga acc	912
aac tgg acc aac acc ctg aag cgc gtg gcc gag aag ctg cgc gag aag	960
ttc aac aac acc acc atc gtg ttc aac cag agc tcc gcc ggc gac ccc	1008
gag atc gtc atg cac agc ttc aac tgc cgc ggc gag ttc ttc tac tgc	1056
aac acc acc cag ctg ttc aac agc acc tgg aac gag acc aac agc gag	1104


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ggc aac atc act agt ggc acc atc acc ctg ccc tgc cgc atc aag cag 1152
atc atc aac atg tgg cag gag gtg ggc aag gcc atg tac gcc ccc ccc 1200
atc ggc ggc cag atc aag tgc ctg agc aac atc acc ggc ctg ctg ctg 1248
acc cgc gac ggc ggc agc gac aac tgg ag 1277

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<210> 50

<211> 425

<212> PRT

<213> Artificial Sequence

<400> 50

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Ala Ser Ala Ala Asp Arg Leu Trp Val Thr Val Tyr Tyr Gly Val Pro
 5 10 15
Val Trp Lys Asp Ala Thr Thr Thr Leu Phe Cys Ala Ser Asp Ala Lys
20 25 30
Ala Tyr Asp Thr Glu Val His Asn Val Trp Ala Thr His Ala Cys Val
35 40 45
Pro Thr Asp Pro Asn Pro Gln Glu Val Val Leu Gly Asn Val Thr Glu
50 55 60
Asn Phe Asn Met Gly Lys Asn Asn Met Val Glu Gln Met His Glu Asp
65 70 75 80
Ile Ile Ser Leu Trp Asp Gln Ser Leu Lys Pro Cys Val Lys Leu Thr
85 90 95
Pro Leu Cys Val Thr Leu Gln Cys Thr Lys Leu Lys Gln Ser Thr Asp
100 105 110
Thr Gln Asn Thr Arg Trp Gly Thr Gln Glu Met Lys Asn Cys Ser Phe
115 120 125
Gln Ile Ser Thr Ser Val Arg Asn Lys Met Lys Arg Glu Tyr Ala Leu
130 135 140
Phe Tyr Ser Leu Asp Ile Val Pro Ile Asp Asn Asp Gln Thr Ser Tyr
145 150 155 160
Arg Leu Arg Ser Cys Asn Thr Ser Ile Ile Thr Gln Ala Cys Pro Lys
165 170 175
Val Ser Phe Glu Pro Ile Pro Ile His Phe Cys Ala Pro Ala Gly Phe
180 185 190
Ala Ile Leu Lys Cys Asn Asn Lys Thr Phe Asn Gly Thr Gly Pro Cys
195 200 205
Thr Asn Val Ser Thr Val Gln Cys Thr His Gly Ile Arg Pro Val Val
210 215 220
Ser Thr Gln Leu Leu Leu Asn Gly Ser Leu Ala Glu Glu Glu Val Val
225 230 235 240
Ile Arg Ser Glu Asn Phe Thr Asn Asn Ala Lys Thr Ile Ile Val Gln
245 250 255
Leu Asn Glu Ser Val Glu Ile Asn Cys Thr Arg Pro Asn Asn Asn Thr
260 265 270
Arg Lys Ser Ile His Ile Gly Pro Gly Arg Ala Phe Tyr Thr Thr Gly
275 280 285
Asp Ile Ile Gly Asp Ile Arg Gln Ala His Cys Asn Ile Ser Arg Thr
290 295 300
Asn Trp Thr Asn Thr Leu Lys Arg Val Ala Glu Lys Leu Arg Glu Lys
305 310 315 320
Phe Asn Asn Thr Thr Ile Val Phe Asn Gln Ser Ser Gly Gly Asp Pro
325 330 335
Glu Ile Val Met His Ser Phe Asn Cys Gly Gly Glu Phe Phe Tyr Cys
340 345 350
Asn Thr Thr Gln Leu Phe Asn Ser Thr Trp Asn Glu Thr Asn Ser Glu
355 360 365
Gly Asn Ile Thr Ser Gly Thr Ile Thr Leu Pro Cys Arg Ile Lys Gln
370 375 380

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Ile Ile Asn Met Trp Gln Glu Val Gly Lys Ala Met Tyr Ala Pro Pro
 385 390 395 400
 Ile Gly Gly Gln Ile Lys Cys Leu Ser Asn Ile Thr Gly Leu Leu Leu
 405 410 415
 Thr Arg Asp Gly Gly Ser Asp Asn Ser
 420 425

210 51

211 144

212 PPT

213 Artificial Sequence

400 51

gct agc gag gcc gac cgc ctg tgg gtg acc gtg tac tac gcc gtg ccc 48
 gtg tgg aag gac gcc acc acc acc ctg ttc tgc gcc agc gac gcc aag 96
 gcc tac gag acc gag gtg cac aac gtg tgg gcc acc cac gcc tgc ctg 144
 ccc acc gag gcc aac ccc cag gag gtg gtg ctg gcc aac gtg acc gag 192
 aac ttc aac aag gcc aag aac aac atg gtg gag cag atg cac gag gat 240
 atc atc agc ctg tgg gac cag agc ctg aag ccc tgc gtg aag ctg acc 288
 ccc ctg tgg gtg acc ctg aac tgc acc aag ctg aag aac agc acc gac 336
 acc aac aac aac cgc tgg gcc acc cag gag atg aag aac tgc agc ttc 384
 cag atc agc aac agc gtg cgc aac aag atg aag cgc gag tac gcc ctg 432
 ttc tac agc ctg gac atc gtg ccc atc gac aac gac cag acc agc tac 480
 cgc ccc cgc aac tgc aac aca tgc atc atc acc cag gcc tgc ccc aag 528
 gtg agc ttc gag ccc atc ccc atc cac ttc tgc gcc ccc gcc ggc ttc 576
 gcc atc ctg aag tgc aac aac aag acc ttc aac gcc acc gcc ccc tgc 624
 acc aac gtg agc acc gtg cag tgc acc cac gga att cgc ccc gtg gtg 672
 agc acc cag ctg ctg ctg aac gcc agc ctg gcc gag gag gag gtg gtg 720
 atc aga ttc gag aac ttc acc aac aac gcc aag acc atc atc gtg cag 768
 ctg aac gag agc gtg gag atc aac tgc acc cgc ccc aac aac aac acc 816
 cgc aag agc atc cac atc gcc cct gcc cgc gcc ttc tac acc acc gcc 864
 gac atc atc gcc gac atc cgc cag gcc cac tgc aac atc ttc aga acc 912
 aac tgg acc aac acc ctg aag cgc gtg gcc gag aag ctg cgc gag aag 960
 ttc aac aac acc acc atc gtg ttc aac cag agc ttc gcc gcc gac ccc 1008
 gag atc gtg aag cac agc ttc aac tgc gcc gcc gag ttc ttc tac tgc 1056
 aac acc acc cag ctg ttc aac agc acc tgg aac gag acc aac agc gag 1104
 gcc aac atc atc agt gcc acc atc acc ctg ccc tgc cgc atc aag cag 1152
 atc atc aac atg tgg cag gag gtg gcc aag gcc atg tac gcc ccc ccc 1200
 atc gcc gcc cag atc aag tgc ctg agc aac atc acc gcc ctg ctg ctg 1248
 acc cgc gac gcc gcc agc gac aac tgc ag 1277

210 51

211 425

212 PPT

213 Artificial Sequence

400 51

Ala Ser Ala Ala Asp Arg Leu Trp Val Thr Val Tyr Tyr Gly Val Pro
 1 5 10 15
 Val Trp Lys Asp Ala Thr Thr Thr Leu Phe Cys Ala Ser Asp Ala Lys
 20 25 30
 Ala Tyr Asp Thr Gln Val His Asn Val Trp Ala Thr His Ala Cys Val
 35 40 45
 Pro Thr Asp Pro Asn Pro Gln Glu Val Val Leu Gly Asn Val Thr Glu
 50 55 60
 Asn Phe Asn Met Gly Lys Asn Asn Met Val Glu Gln Met His Glu Asp
 65 70 75 80
 Ile Ile Ser Leu Trp Asp Gln Ser Leu Lys Pro Cys Val Lys Leu Thr
 85 90 95

Pro Leu Cys Val Thr Leu Asn Cys Thr Lys Leu Lys Asn Ser Thr Asp
 100 105 110
 Thr Asn Asn Thr Arg Trp Gly Thr Gln Glu Met Lys Asn Cys Ser Phe
 115 120 125
 Gln Ile Ser Thr Ser Val Arg Asn Lys Met Lys Arg Glu Tyr Ala Leu
 130 135 140
 Phe Tyr Ser Leu Asp Ile Val Pro Ile Asp Asn Asp Gln Thr Ser Tyr
 145 150 155 160
 Arg Leu Arg Ser Cys Asn Thr Ser Ile Ile Thr Gln Ala Cys Pro Lys
 165 170 175
 Val Ser Phe Glu Pro Ile Pro Ile His Phe Cys Ala Pro Ala Gly Phe
 180 185 190
 Ala Ile Leu Lys Cys Asn Asn Lys Thr Phe Asn Gly Thr Gly Pro Cys
 195 200 205
 Thr Asn Val Ser Thr Val Gln Cys Thr His Gly Ile Arg Pro Val Val
 210 215 220
 Ser Thr Gln Leu Leu Leu Asn Gly Ser Leu Ala Glu Glu Glu Val Val
 225 230 235 240
 Ile Arg Ser Glu Asn Phe Thr Asn Asn Ala Lys Thr Ile Ile Val Gln
 245 250 255
 Leu Asn Glu Ser Val Glu Ile Asn Cys Thr Arg Pro Asn Asn Thr
 260 265 270
 Arg Lys Ser Ile His Ile Gly Pro Gly Arg Ala Phe Tyr Thr Thr Gly
 275 280 285
 Asp Ile Ile Gly Asp Ile Arg Gln Ala His Cys Asn Ile Ser Arg Thr
 290 295 300
 Asn Trp Thr Asn Thr Leu Lys Arg Val Ala Glu Lys Leu Arg Glu Lys
 305 310 315 320
 Phe Asn Asn Thr Thr Ile Val Phe Asn Gln Ser Ser Gly Gly Asp Pro
 325 330 335
 Glu Ile Val Met His Ser Phe Asn Cys Gly Gly Glu Phe Phe Tyr Cys
 340 345 350
 Asn Thr Thr Gln Leu Phe Asn Ser Thr Trp Asn Glu Thr Asn Ser Glu
 355 360 365
 Gly Asn Ile Thr Ser Gly Thr Ile Thr Leu Pro Cys Arg Ile Lys Gln
 370 375 380
 Ile Ile Asn Met Trp Gln Glu Val Gly Lys Ala Met Tyr Ala Pro Pro
 385 390 395 400
 Ile Gly Gly Gln Ile Lys Cys Leu Ser Asn Ile Thr Gly Leu Leu Leu
 405 410 415
 Thr Arg Asp Gly Gly Ser Asp Asn Ser
 420 425

<210> 53

<211> 432

<212> DNA

<213> Artificial Sequence

<220>

<221> CDS

<222> (1)...(432)

<400> 53

tat aga ggc cta cct cca gga cca ggc att cct ggg cat ctg ggg ctg
 Ser Arg Ala Leu Pro Gly Pro Ala Leu Pro Gly His Val Gly Leu
 1 5 10 15

ctg cgg caa gat gat ctg cac cac ggc cgt gcc ctg gaa cgc cag ctg
 Leu Arg Gln Ala Asp Leu His His Gly Arg Ala Leu Glu Arg Gln Leu

20	25	30	
gag caa caa gaa cct gag cca gat ttg gga caa cat gac ctg gat gga Glu Gln Gln Glu Pro Glu Pro Asp Leu Gly Gln His Asp Leu Asp Gly 35 40 45			144
gtg gga gag cga gat cag caa cta cac cga gat cat cta cag cct gat Val Gly Ala Arg Asp Gln Gln Leu His Arg Asp His Leu Gln Pro Asp 50 55 60			192
cga gga gag cca gaa cca gca gga gaa caa cga gct gga cct gct cca Arg Gly Gln Pro Glu Pro Ala Gly Gln Gln Arg Ala Gly Pro Ala Pro 65 70 75 80			240
gct gga caa gng ggc aag ctt gtg gaa ctg gtt caa cat cac caa ctg Ala Gly Gln Val Gly Lys Leu Val Glu Leu Val Gln His His Gln Leu 85 90 95			288
gct gtg gta cat caa gat ttt cat cat gat cgt ggg cgg cct gat cgg Ala Val Val His Gln Asp Phe His His Asp Arg Gly Arg Pro Asp Arg 100 105 110			336
cct gag cat cgt gtt cac cgt gct gag cat cgt gaa cgg cgt gcg cca Pro Ala His Arg Val His Arg Ala Glu His Arg Glu Pro Arg Ala Pro 115 120 125			384
ggg cta cag ccc cct gag ctt cca gac ccg cct gcc cgt gcc cgg cgg Gly Leu Gln Pro Pro Glu Leu Pro Asp Pro Pro Ala Arg Ala Pro Arg 130 135 140			432

<210> 54

<211> 144

<212> PRT

<213> Artificial Sequence

<400> 54

Ser Arg Ala Leu Pro Pro Gly Pro Ala Leu Pro Gly His Val Gly Leu
1 5 10 15
Leu Arg Gln Ala Asp Leu His His Gly Arg Ala Leu Glu Arg Gln Leu
20 25 30
Glu Gln Gln Glu Pro Glu Pro Asp Leu Gly Gln His Asp Leu Asp Gly
35 40 45
Val Gly Ala Arg Asp Gln Gln Leu His Arg Asp His Leu Gln Pro Asp
50 55 60
Arg Gly Glu Pro Glu Pro Ala Gly Glu Glu Arg Ala Gly Pro Ala Pro
65 70 75 80
Ala Gly Gln Val Gly Lys Leu Val Glu Leu Val Gln His His Gln Leu
85 90 95
Ala Val Val His Gln Asp Phe His His Asp Arg Gly Arg Pro Asp Arg
100 105 110
Pro Ala His Arg Val His Arg Ala Glu His Arg Glu Pro Arg Ala Pro
115 120 125
Gly Met Gln Pro Pro Glu Leu Pro Asp Pro Pro Ala Arg Val Thr Asp
130 135 140

<210> 55

<211> 434

<212> DNA

2213> Artificial Sequence

2220>

2221> CDS

2222> (1)...(434)

4000> 55

tot aga cgg cta cct cca gga cca gcg ctt cct ggg cat gtg ggg ctg 48
 Ser Arg Ala Leu Pro Pro Gly Pro Ala Leu Pro Gly His Val Gly Leu
 1 5 10 15

ctc cgg caa gct gat ctg cac cac ggc cgt gcc ctg gaa cgc gag ctg 96
 Leu Arg Gln Ala Asp Leu His His Gly Arg Ala Leu Glu Arg Gln Leu
 20 25 30

gag caa caa gaa cct gag cca gat ttg gga caa cat gac ctg gat gga 144
 Glu Gln Gln Glu Pro Glu Pro Asp Leu Gly Gln His Asp Leu Asp Gly
 35 40 45

gtg gga gcg cga gat cag caa cta cac cga gat cat cta gag cct gat 192
 Val Gly Ala Arg Asp Gln Gln Leu His Arg Asp His Leu Gln Pro Asp
 50 55 60

cga gga gag cca gaa cca gca gga gaa gaa cga gct gga cct gct cca 240
 Arg Gly Gln Pro Glu Pro Ala Gly Glu Glu Arg Ala Gly Pro Ala Pro
 65 70 75 80

gct gga caa gtg ggc aag ctt gtg gaa ctg gtt caa cat cac caa ctg 288
 Ala Gly Gln Val Gly Lys Leu Val Glu Leu Val Gln His His Gln Leu
 85 90 95

gct gta gta cat caa gat ttt cat cat gat cgt ggg cgg cct gat cgg 336
 Ala Val Val His Gln Asp Phe His His Asp Arg Gly Arg Pro Asp Arg
 100 105 110

cct gga cat cgt gtt cac cgt gct gag cat cgt gaa cgg cgt ggg cca 384
 Pro Ala His Arg Val His Arg Ala Glu His Arg Glu Pro Arg Ala Pro
 115 120 125

ggg atg gag ccc cct gag ctt cca gac cgg cct gcc cgt gtg aag gat 432
 Gly Met Gln Pro Pro Glu Leu Pro Asp Pro Pro Ala Arg Val Thr Asp
 130 135 140

cc 434

2100> 56

2110> 144

2120> PFT

2130> Artificial Sequence

4000> 56

Ser Arg Ala Leu Pro Pro Gly Pro Ala Leu Pro Gly His Val Gly Leu
 1 5 10 15
 Leu Arg Gln Ala Asp Leu His His Gly Arg Ala Leu Glu Arg Gln Leu
 20 25 30
 Glu Gln Gln Glu Pro Glu Pro Asp Leu Gly Gln His Asp Leu Asp Gly
 35 40 45
 Val Gly Ala Arg Asp Gln Gln Leu His Arg Asp His Leu Gln Pro Asp
 50 55 60

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Arg Gly Glu Pro Glu Pro Ala Gly Glu Glu Arg Ala Gly Pro Ala Pro
65                      70                      75                      80
Ala Gly Gln Val Gly Lys Leu Val Glu Leu Val Gln His His Gln Leu
                      85                      90                      95
Ala Val Val His Gln Asp Phe His His Asp Arg Gly Arg Pro Asp Arg
100                      105                      110
Pro Ala His Arg Val His Arg Ala Glu His Arg Glu Pro Arg Ala Pro
115                      120                      125
Gly Met Gln Pro Pro Glu Leu Pro Asp Pro Pro Ala Arg Val Thr Asp
130                      135                      140

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<210> 57
<211> 231
<212> DNA
<213> Artificial Sequence

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<220>
<221> CDS
<222> (1)...(281)

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400> 57
tot aga gag cta cct cca gga cca gcg ctt cct ggg cat gtg ggg ctg      48
Ser Arg Ala Leu Pro Pro Gly Pro Ala Leu Pro Gly His Val Gly Leu
1                      5                      10                      15
ctc cgg caa gct gat ctg cac cac ggc cgt gcc ctg gaa cgc cag ctg      96
Leu Arg Gln Ala Asp Leu His His Gly Arg Ala Leu Glu Arg Gln Leu
20                      25                      30
gag caa caa gaa cct gag cca gat ttg gga caa cat gac ctg gat gga      144
Glu Gln Gln Glu Pro Glu Pro Asp Leu Gly Gln His Asp Leu Asp Gly
35                      40                      45
gtg gga gag cta gat cag caa cta caa cga gat cat cta cag cct gat      192
Val Gly Ala Arg Asp Gln Gln Leu His Arg Asp His Leu Gln Pro Asp
50                      55                      60
cga gga gag cta gaa cca gca gga gaa gaa cga gct gga cct gct cca      240
Arg Gly Glu Pro Glu Pro Ala Gly Glu Glu Arg Ala Gly Pro Ala Pro
65                      70                      75                      80
gct gga caa gtg ggc aag ctt gtg tga ctg att gag gat cc      281
Ala Gly Gln Val Gly Lys Leu Val * Leu Ile Glu Asp
85                      90

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```

<210> 58
<211> 91
<212> PPT
<213> Artificial Sequence

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400> 58
Ser Arg Ala Leu Pro Pro Gly Pro Ala Leu Pro Gly His Val Gly Leu
1                      5                      10                      15
Leu Arg Gln Ala Asp Leu His His Gly Arg Ala Leu Glu Arg Gln Leu
20                      25                      30
Glu Gln Gln Glu Pro Glu Pro Asp Leu Gly Gln His Asp Leu Asp Gly
35                      40                      45
Val Gly Ala Arg Asp Gln Gln Leu His Arg Asp His Leu Gln Pro Asp

```

50					55					60					
Arg	Gly	Glu	Pro	Glu	Pro	Ala	Gly	Glu	Glu	Arg	Ala	Gly	Pro	Ala	Pro
65					70					75					80
Ala	Gly	Gln	Val	Gly	Lys	Leu	Val	Leu	Ile	Glu	Asp				
				85					90						

```

<210> 59
<211> 272
<212> DNA
<213> Artificial Sequence

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0220:
0221: CDS
0222: (1) ... (272)

4400- 59																		
atc gat tgc ggc acc tgc tgc tga tgc tgg ccc gca tgc tgg agc tgc	48																	
Ile Asp Cys Ala Thr Cys Cys * Ser Trp Pro Ala Ser Trp Ser Cys																		
1 5 10 15																		
tgg gcc ggc ggc att ggg aga tcc tga agt act ggt gga acc tgc tcc	96																	
Trp Ala Gly Ala Ala Gly Arg Ser * Ser Thr Gly Gly Thr Cys Ser																		
20 25 30																		
agt act gga gcc agg agc tga aga act ctg cag tga gcc tgc tga acg	144																	
Ser Thr Gly Ala Arg Ser * Arg Thr Leu Gln * Ala Cys * Thr																		
35 40																		
cca ccg cca tgc ccg tgg ccg agg gca ccg acc gcg tga tgc agg tgg	192																	
Pro Pro Pro Ser Pro Trp Pro Arg Ala Pro Thr Ala * Ser Arg Trp																		
45 50 55																		
tgc agc gca tct ggc gcg gca tcc tgc aca tcc cca ccc gaa ttc gcc	240																	
Cys Ser Ala Ser Gly Ala Ala Ser Cys Thr Ser Pro Pro Glu Phe Ala																		
60 65 70																		
agg gct tcg agc gcg ccc tgc tgt aag gat cc	272																	
Arg Ala Ser Ser Ala Pro Cys Cys Lys Asp																		
75 80																		

0210 . 60
0211 . 84
0212 . PRT
0213 . Artificial Sequence

[illegible]

<210> 61
 <211> 798
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> CDS
 <222> (1)...(798)

<400> 61

ctc gag cag cgg caa gga gat ttt ccg ccc cgg cgg cgg cga cat gcg	48
Leu Gln Gln Arg Gln Gly Asp Phe Pro Pro Arg Arg Arg Arg His Ala	
1 5 10 15	
cga caa ctc ggc cag cga gct gta caa gta caa ggt ggt gaa gat cga	96
Arg Gln Leu Ala Gln Arg Ala Val Gln Val Gln Gly Gly Glu Asp Arg	
20 25 30	
gca ccc ggc cat cgc ccc cac caa ggc caa ggc cgc cgt ggt gca gcg	144
Ala Pro Gly His Arg Pro His Gln Gly Gln Ala Pro Arg Gly Ala Ala	
35 40 45	
cga gaa ggc cgc cgt ggg cat cgg cgc tat gtt cct cgg ctt cct gcg	192
Arg Gln Ala Arg Arg Gly His Arg Arg Tyr Val Pro Arg Leu Pro Gly	
50 55 60	
cgc tga agg cag cac cat ggg cgc cgc cag cct gac cct gac cgt gca	240
Arg Cys Arg Gln His His Gly Arg Arg Gln Pro Asp Pro Asp Arg Ala	
65 70 75 80	
ggc ccc cca gct gct gag cgg cat cgt gca gca gca gaa caa cct gct	288
Gly Pro Pro Ala Ala Glu Arg His Arg Ala Ala Ala Glu Gln Pro Ala	
85 90 95	
ggc cgc cat cga ggc cca gca gca cct gct cca gct gac cgt gtg ggc	336
Ala Arg His Arg Gly Pro Ala Ala Pro Ala Pro Ala Asp Arg Val Gly	
100 105 110	
cat caa gca gct cca ggc ccg cgt gct ggc tat aga gcg cta cct cca	384
His Gln Ala Ala Pro Gly Pro Arg Ala Gly Ser Arg Ala Leu Pro Pro	
115 120 125	
gga cca ggc ctt cct ggg cat gtg ggc ctg ctc cgg caa gct gat ctg	432
Gly Pro Ala Leu Pro Gly His Val Gly Leu Leu Arg Gln Ala Asp Leu	
130 135 140	
cac cac ggc cgt gcc ctg gaa cgc cag ctg gag caa caa gaa cct gag	480
His His Gly Arg Ala Leu Glu Arg Gln Leu Glu Gln Gln Glu Pro Glu	
145 150 155 160	
cca gat ttg gga caa cat gac ctg gat gga gtg gga gcg cga gat cag	528
Pro Asp Leu Gly Gln His Asp Leu Asp Gly Val Gly Ala Arg Asp Gln	
165 170 175	
caa cta cac cga gat cat cta cag cct gat cga gga gag cca gaa cca	576
Gln Leu His Arg Asp His Leu Gln Pro Asp Arg Gly Glu Pro Glu Pro	
180 185 190	

gca gga gaa gaa cga gct gga cct gct cca gct gga caa gtg ggc aag 624
 Ala Gly Glu Glu Arg Ala Gly Pro Ala Pro Ala Gly Gln Val Gly Lys
 195 200 205
 cct gtt gaa ctg gtt caa cat cac caa ctg gct gtg gta cat caa gat 672
 Leu Val Glu Leu Val Gln His His Gln Leu Ala Val Val His Gln Asp
 210 215 220
 ttt cat cat gat cgt ggg cgg cct gat cgg cct ggg cat cgt gtt cac 720
 Phe His His Asp Arg Gly Arg Pro Asp Arg Pro Ala His Arg Val His
 225 230 235 240
 cgt gct gag cat cgt gaa ccg cgt ggg cca ggg cta cag ccc cct gag 768
 Arg Ala Glu His Arg Glu Pro Arg Ala Pro Gly Leu Gln Pro Pro Glu
 245 250 255
 ctt cca gag cag cct gct cgt gct cgt cgg 796
 Leu Pro Asp Pro Pro Ala Arg Ala Pro Arg
 260 265

210 62

211 266

212 PRT

213 Artificial Sequence

400 62

Leu Glu Gln Arg Gln Gly Asp Phe Pro Pro Arg Arg Arg Arg His Ala
 1 5 10 15
 Arg Gln Leu Ala Gln Arg Ala Val Gln Val Gln Gly Gly Glu Asp Arg
 20 25 30
 Ala Pro Gly His Arg Pro His Gln Gly Gln Ala Pro Arg Gly Ala Ala
 35 40 45
 Arg Glu Ala Arg Arg Gly His Arg Arg Tyr Val Pro Arg Leu Pro Gly
 50 55 60
 Arg Cys Arg Gln His His Gly Arg Arg Gln Pro Asp Pro Asp Arg Ala
 65 70 75 80
 Gly Pro Pro Ala Ala Glu Arg His Arg Ala Ala Ala Glu Gln Pro Ala
 85 90 95
 Ala Arg His Arg Gly Pro Ala Ala Pro Ala Pro Ala Asp Arg Val Gly
 100 105 110
 His Gln Ala Ala Pro Gly Pro Arg Ala Gly Ser Arg Ala Leu Pro Pro
 115 120 125
 Gly Pro Ala Leu Pro Gly His Val Gly Leu Leu Arg Gln Ala Asp Leu
 130 135 140
 His His Gly Arg Ala Leu Glu Arg Gln Leu Glu Gln Gln Glu Pro Glu
 145 150 155 160
 Pro Asp Leu Gly Gln His Asp Leu Asp Gly Val Gly Ala Arg Asp Gln
 165 170 175
 Gln Leu His Arg Asp His Leu Gln Pro Asp Arg Gly Glu Pro Glu Pro
 180 185 190
 Ala Gly Gln Glu Arg Ala Gly Pro Ala Pro Ala Gly Gln Val Gly Lys
 195 200 205
 Leu Val Gln Leu Val Gln His His Gln Leu Ala Val Val His Gln Asp
 210 215 220
 Phe His His Asp Arg Gly Arg Pro Asp Arg Pro Ala His Arg Val His
 225 230 235 240
 Arg Ala Glu His Arg Glu Pro Arg Ala Pro Gly Leu Gln Pro Pro Glu
 245 250 255

Leu Pro Asp Pro Pro Ala Arg Ala Pro Arg
260 265

<210> 63
<211> 900
<212> DNA
<213> Artificial Sequence

<220>
<221> CDS
<222> (1)...(900)

<400> 63

ctc gaa cag cgg caa gga gat ttt ccg ccc cgg cgg cgg cga cat ggc	48
Leu Gln Gln Arg Gln Gly Asp Phe Pro Pro Arg Arg Arg Arg His Ala	
1 5 10 15	
cga caa ctg gag cag cga gct gta caa gta caa ggt ggt gaa gat cga	96
Arg Gln Leu Ala Gln Arg Ala Val Gln Val Gln Gly Gly Glu Asp Arg	
20 25 30	
gcc cct ggg cat cgc ccc ccc caa ggc caa ggc ccg cgt ggt gca ggc	144
Ala Pro Gly His Arg Pro His Gln Gly Gln Ala Pro Arg Gly Ala Ala	
35 40 45	
cga gaa ggc cgc cgt ggg cat cgg cgc tat gtt cct cgg ctt cct ggc	192
Arg Glu Ala Arg Arg Gly His Arg Arg Tyr Val Pro Arg Leu Pro Gly	
50 55 60	
cgc tgc agg cag cac cat ggg cgc cgc cag cct gac cct gac cgt gca	240
Arg Cys Arg Gln His His Gly Arg Arg Gln Pro Asp Pro Asp Arg Ala	
65 70 75 80	
ggc cag cca gct gct gag cgg cat cgt gca gca gca gaa caa cct gct	288
Gly Pro Pro Ala Ala Gln Arg His Arg Ala Ala Ala Glu Gln Pro Ala	
85 90 95	
ggc cgc cat cga ggc cca gca gca cct gct cca gct gac cgt gtg ggc	336
Ala Arg His Arg Gly Pro Ala Ala Pro Ala Pro Ala Asp Arg Val Gly	
100 105 110	
cat caa gca gct cca ggc ccg cgt gct ggc tat aga ggc cta cct cca	384
His Gln Ala Ala Pro Gly Pro Arg Ala Gly Ser Arg Ala Leu Pro Pro	
115 120 125	
gga cca ggc ctt cct ggg cat gtg ggc ctg ctg cgg caa gct gat ctg	432
Gly Pro Ala Leu Pro Gly His Val Gly Leu Leu Arg Gln Ala Asp Leu	
130 135 140	
cac cac ggc cgt gcc ctg gaa cgc cag ctg gag caa caa gaa cct gag	480
His His Gly Arg Ala Leu Glu Arg Gln Leu Glu Gln Gln Glu Pro Glu	
145 150 155 160	
cca gat tgg gga caa cat gac ctg gat gga gtg gga ggc cga gat gag	528
Pro Asp Leu Gly Gln His Asp Leu Asp Gly Val Gly Ala Arg Asp Gln	
165 170 175	
caa cta cac cga cat cat cta cag cct gat cga gga gag cca gaa cca	576
Gln Leu His Arg Asp His Leu Gln Pro Asp Arg Gly Glu Pro Glu Pro	

180	185	190	
gca gga gaa gaa cga gct gga cct gct cca gct gga caa gtg ggc aag			624
Ala Gly Glu Glu Arg Ala Gly Pro Ala Pro Ala Gly Gln Val Gly Lys			
135	200	205	
cct gtg gaa ctg gtt caa cat cac caa ctg gct gtg gta cat caa gat			672
Leu Val Glu Leu Val Gln His His Gln Leu Ala Val Val His Gln Asp			
210	215	220	
ttt cat cat gat cgt ggg cgg cct gat cgg cct ggg cat cgt gtt cac			720
Phe His His Asp Arg Gly Arg Pro Asp Arg Pro Ala His Arg Val His			
225	230	235	240
cgt gct gag cat cgt gaa cgg cgt ggg cca ggg atg caa ccc cct gag			768
Arg Ala Glu His Arg Glu Pro Arg Ala Pro Gly Met Gln Pro Pro Glu			
245	250	255	
cct cca gac cgg cct gac cgt gtg acg gat cc			800
Leu Pro Asp Pro Pro Ala Arg Val Thr Asp			
260	265		

<210> 64

<211> 266

<212> PRT

<213> Artificial Sequence

<400> 64

Leu	Glu	Gln	Arg	Gln	Gly	Asp	Phe	Pro	Pro	Arg	Arg	Arg	Arg	His	Ala
1				5					10					15	
Arg	Gln	Leu	Ala	Gln	Arg	Ala	Val	Gln	Val	Gln	Gly	Gly	Glu	Asp	Arg
		20						25					30		
Ala	Pro	Gly	His	Arg	Pro	His	Gln	Gly	Gln	Ala	Pro	Arg	Gly	Ala	Ala
	35					40						45			
Arg	Glu	Ala	Arg	Arg	Gly	His	Arg	Arg	Tyr	Val	Pro	Arg	Leu	Pro	Gly
	50					55					60				
Arg	Cys	Arg	Gln	His	His	Gly	Arg	Arg	Gln	Pro	Asp	Pro	Asp	Arg	Ala
	65				70					75				80	
Gly	Pro	Pro	Ala	Ala	Glu	Arg	His	Arg	Ala	Ala	Ala	Glu	Gln	Pro	Ala
			85						90					95	
Ala	Arg	His	Arg	Gly	Pro	Ala	Ala	Pro	Ala	Pro	Ala	Asp	Arg	Val	Gly
		100						105					110		
His	Gln	Ala	Ala	Pro	Gly	Pro	Arg	Ala	Gly	Ser	Arg	Ala	Leu	Pro	Pro
	115						120					125			
Gly	Pro	Ala	Leu	Pro	Gly	His	Val	Gly	Leu	Leu	Arg	Gln	Ala	Asp	Leu
	130					135					140				
His	His	Gly	Arg	Ala	Leu	Glu	Arg	Gln	Leu	Glu	Gln	Gln	Glu	Pro	Glu
	145				150					155				160	
Pro	Asp	Leu	Gly	Gln	His	Asp	Leu	Asp	Gly	Val	Gly	Ala	Arg	Asp	Gln
			165						170					175	
Gln	Leu	His	Arg	Asp	His	Leu	Gln	Pro	Asp	Arg	Gly	Glu	Pro	Glu	Pro
		180						185					190		
Ala	Gly	Glu	Glu	Arg	Ala	Gly	Pro	Ala	Pro	Ala	Gly	Gln	Val	Gly	Lys
	195						200						205		
Leu	Val	Glu	Leu	Val	Gln	His	Gln	Leu	Ala	Val	Val	His	Gln	Asp	
	210					215					220				
Phe	His	His	Asp	Arg	Gly	Arg	Pro	Asp	Arg	Pro	Ala	His	Arg	Val	His
	225					230					235				240

Arg Ala Glu His Arg Glu Pro Arg Ala Pro Gly Met Gln Pro Pro Glu
 245 250 255
 Leu Pro Asp Pro Pro Ala Arg Val Thr Asp
 260 265

<210> 65
 <211> 647
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> CDS
 <222> (1)...(647)

<400> 65
 ctc gag cag cgg caa gga gat ttt ccg ccc cgg cgg cgg cga cat gcg 48
 Leu Glu Gln Arg Gln Gly Asp Phe Pro Pro Arg Arg Arg Arg His Ala
 1 5 10 15
 cga caa ctg ggg cag cga gct gta caa gta caa ggt ggt gaa gat cga 96
 Arg Gln Leu Ala Gln Arg Ala Val Gln Val Gln Gly Gly Glu Asp Arg
 20 25 30
 gcc cct ggg cat cgc ccc cac caa ggc caa gcg ccg cgt ggt gca gcg 144
 Ala Pro Gly His Arg Pro His Gln Gly Gln Ala Pro Arg Gly Ala Ala
 35 40 45
 cga gaa gcg cgc cgt ggg cat cgg cgc tat gtt cct cgg ctt cct ggg 192
 Arg Glu Ala Arg Arg Gly His Arg Arg Tyr Val Pro Arg Leu Pro Gly
 50 55 60
 cgc tgc agg cag cac cat ggg cgc cgc cag cct gac cct gac cgt gca 240
 Arg Cys Arg Gln His His Gly Arg Arg Gln Pro Asp Pro Asp Arg Ala
 65 70 75 80
 ggc ccg cca gct gct gag cgg cat cgt gca gca cca gaa caa cct gct 288
 Gly Pro Pro Ala Ala Glu Arg His Arg Ala Ala Ala Glu Gln Pro Ala
 85 90 95
 ggc cgc cat cga ggc cca gca gca cct gct cca gct gac cgt gtg ggg 336
 Ala Arg His Arg Gly Pro Ala Ala Pro Ala Pro Ala Asp Arg Val Gly
 100 105 110
 cat caa gca gct cca ggc ccg cgt gct ggc tct aga gcg cta cct cca 384
 His Gln Ala Ala Pro Gly Pro Arg Ala Gly Ser Arg Ala Leu Pro Pro
 115 120 125
 gga cca gcg ctt cct ggg cat gtg ggg ctg ctg cgg caa gct gat ctg 432
 Gly Pro Ala Leu Pro Gly His Val Gly Leu Leu Arg Gln Ala Asp Leu
 130 135 140
 cac cac ggc cgt gcc ctg gaa cgc cag ctg gag caa caa gaa cct gag 480
 His His Gly Arg Ala Leu Glu Arg Gln Leu Glu Gln Gln Glu Pro Glu
 145 150 155 160
 cca gat ttg gga caa cat gac ctg gat gga ctg gga gcg cga gat cag 516
 Pro Asp Leu Gly Gln His Asp Leu Asp Gly Val Gly Ala Arg Asp Gln
 165 170 175

caa cta cac cga gat cat cta cag cct gat cga gga gag cca gaa cca 576
Gln Leu His Arg Asp His Leu Gln Pro Asp Arg Gly Glu Pro Glu Pro
180 185 190

gca gga gaa gaa cga gct gga cct gct cca gct gga caa gtg ggc aag 624
Ala Gly Glu Glu Arg Ala Gly Pro Ala Pro Ala Gly Gln Val Gly Lys
195 200 205

ctt gtg tga ctg att gag gat cc 647
Leu Val * Leu Ile Glu Asp
210

<210> 66
<211> 214
<212> PRT
<213> Artificial Sequence

<400> 66
Leu Gln Gln Arg Gln Gly Asp Phe Pro Pro Arg Arg Arg Arg His Ala
1 5 10 15
Arg Gln Leu Ala Gln Arg Ala Val Gln Val Gln Gly Gly Glu Asp Arg
20 25 30
Ala Pro Gly His Arg Pro His Gln Gly Gln Ala Pro Arg Gly Ala Ala
35 40 45
Arg Glu Ala Arg Arg Gly His Arg Arg Tyr Val Pro Arg Leu Pro Gly
50 55 60
Arg Cys Arg Gln His His Gly Arg Arg Gln Pro Asp Pro Asp Arg Ala
65 70 75 80
Gly Pro Pro Ala Ala Glu Arg His Arg Ala Ala Ala Glu Gln Pro Ala
85 90 95
Ala Arg His Arg Gly Pro Ala Ala Pro Ala Pro Ala Asp Arg Val Gly
100 105 110
His Gln Ala Ala Pro Gly Pro Arg Ala Gly Ser Arg Ala Leu Pro Pro
115 120 125
Gly Pro Ala Leu Pro Gly His Val Gly Leu Leu Arg Gln Ala Asp Leu
130 135 140
His His Gly Arg Ala Leu Glu Arg Gln Leu Glu Gln Gln Glu Pro Glu
145 150 155 160
Pro Asp Leu Gly Gln His Asp Leu Asp Gly Val Gly Ala Arg Asp Gln
165 170 175
Gln Leu His Arg Asp His Leu Gln Pro Asp Arg Gly Glu Pro Glu Pro
180 185 190
Ala Gly Glu Glu Arg Ala Gly Pro Ala Pro Ala Gly Gln Val Gly Lys
195 200 205
Leu Val Leu Ile Glu Asp
210

<210> 67
<211> 1918
<212> DNA
<213> Artificial Sequence

<220>
<221> CDS
<222> (1)...(1918)

<400> 67
gat agc gag gcc gac cgc ctg tgg gtg acc gtg tac tac gac gtg ccc

Ala	Ser	Ala	Ala	Asp	Arg	Leu	Trp	Val	Thr	Val	Tyr	Tyr	Gly	Val	Pro	
1				5					10					15		
gtg	tgg	aag	gac	goc	acc	acc	acc	ctg	tto	tgc	goc	agc	gac	goc	aag	96
Val	Trp	Lys	Asp	Ala	Thr	Thr	Thr	Leu	Phe	Cys	Ala	Ser	Asp	Ala	Lys	
			20					25					30			
goc	tac	gac	acc	gag	gtg	bac	aac	gtg	tgg	goc	acc	cac	gog	tgc	gtg	144
Ala	Tyr	Asp	Thr	Glu	Val	His	Asn	Val	Trp	Ala	Thr	His	Ala	Cys	Val	
			35				40					45				
acc	acc	gac	ccc	aac	ccc	cag	gag	gtg	gtg	ctg	ggc	aac	gtg	acc	gag	192
Pro	Thr	Asp	Pro	Asn	Pro	Gln	Glu	Val	Val	Leu	Gly	Asn	Val	Thr	Glu	
			50			55					60					
aac	tto	aac	atg	ggc	aag	aac	aac	atg	gtg	gag	cag	atg	bac	gag	gat	240
Asn	Phe	Asn	Met	Gly	Lys	Asn	Asn	Met	Val	Glu	Gln	Met	His	Glu	Asp	
	65				70				75					80		
atc	atc	agc	ctg	tgg	gac	cag	agc	ctg	aag	ccc	tgc	gtg	aag	ctg	acc	288
Ile	Ile	Ser	Leu	Trp	Asp	Gln	Ser	Leu	Lys	Pro	Cys	Val	Lys	Leu	Thr	
			85					90					95			
ccc	ctg	tgc	gtg	acc	ctg	aac	tgc	acc	aag	ctg	aag	aac	agc	acc	gac	336
Pro	Leu	Cys	Val	Thr	Leu	Asn	Cys	Thr	Lys	Leu	Lys	Asn	Ser	Thr	Asp	
			100					105					110			
acc	aac	aac	acc	cgc	tgg	ggc	acc	cag	gag	atg	aag	aac	tgc	agc	tto	384
Thr	Asn	Asn	Thr	Arg	Trp	Gly	Thr	Gln	Glu	Met	Lys	Asn	Cys	Ser	Phe	
			115				120						125			
aac	atc	agc	acc	agc	gtg	cgc	aac	aag	atg	aag	cgc	gag	tac	goc	ctg	432
Asn	Ile	Ser	Thr	Ser	Val	Arg	Asn	Lys	Met	Lys	Arg	Glu	Tyr	Ala	Leu	
	130					135					140					
tto	tac	agc	ctg	gac	atc	gtg	ccc	atc	gac	aac	gac	aac	acc	agc	tac	480
Phe	Tyr	Ser	Leu	Asp	Ile	Val	Pro	Ile	Asp	Asn	Asp	Asn	Thr	Ser	Tyr	
	145				150				155						160	
cgc	ctg	cgc	agc	tgc	aac	aca	tgc	atc	atc	acc	cag	goc	tgc	ccc	aag	528
Arg	Leu	Arg	Ser	Cys	Asn	Thr	Ser	Ile	Ile	Thr	Gln	Ala	Cys	Pro	Lys	
			165					170					175			
gtg	agc	tto	gag	ccc	atc	ccc	atc	cac	tto	tgc	goc	ccc	goc	ggc	tto	576
Val	Ser	Phe	Glu	Pro	Ile	Pro	Ile	His	Phe	Cys	Ala	Pro	Ala	Gly	Phe	
			180					185					190			
goc	atc	ctg	aag	tgc	aac	aac	aag	acc	tto	aac	ggc	acc	ggc	ccc	tgc	624
Ala	Ile	Leu	Lys	Cys	Asn	Asn	Lys	Thr	Phe	Asn	Gly	Thr	Gly	Pro	Cys	
			195				200						205			
acc	aac	gtg	agc	acc	gtg	cag	tgc	acc	ccc	gga	att	cgc	ccc	gtg	gtg	672
Thr	Asn	Val	Ser	Thr	Val	Gln	Cys	Thr	His	Gly	Ile	Arg	Pro	Val	Val	
			210			215						220				
agc	acc	cag	ctg	ctg	ctg	aac	ggc	agc	ctg	goc	gag	gag	gag	gtg	gtg	
Ser	Thr	Gln	Leu	Leu	Leu	Asn	Gly	Ser	Leu	Ala	Glu	Glu	Glu	Val	Val	
	225				230					235				240		

atc aga tct gag aac ttc acc aac aac gcc aag acc atc atc gtg cag Ile Arg Ser Glu Asn Phe Thr Asn Asn Ala Lys Thr Ile Ile Val Gln 245 250 255	768
ctg aac gag agc gtg gag atc aac tgc acc cgc ccc aac aac aac acc Leu Asn Glu Ser Val Glu Ile Asn Cys Thr Arg Pro Asn Asn Asn Thr 260 265 270	816
cgc aag agc atc cac atc ggc cct ggc cgc gcc ttc tac acc acc ggc Arg Lys Ser Ile His Ile Gly Pro Gly Arg Ala Phe Tyr Thr Thr Gly 275 280 285	864
gac atc atc ggc gac atc cgc cag gcc cac tgc aac atc tct aga acc Asp Ile Ile Gly Asp Ile Arg Gln Ala His Cys Asn Ile Ser Arg Thr 290 295 300	912
aac tgg acc aac acc ctg aag cgc gtg gcc gag aag ctg cgc gag aag Asn Trp Thr Asn Thr Leu Lys Arg Val Ala Glu Lys Leu Arg Glu Lys 305 310 315 320	960
ttc aac aac acc acc atc gtg ttc aac cag agc tcc ggc ggc gac ccc Phe Asn Asn Thr Thr Ile Val Phe Asn Gln Ser Ser Gly Gly Asp Pro 325 330 335	1008
gag atc gtg atg cac agc ttc aac tgc ggc ggc gag ttc ttc tac tgc Glu Ile Val Met His Ser Phe Asn Cys Gly Gly Glu Phe Phe Tyr Cys 340 345 350	1056
aac acc acc cag ctg ttc aac agc acc tgg aac gag acc aac agc gag Asn Thr Thr Gln Leu Phe Asn Ser Thr Trp Asn Glu Thr Asn Ser Glu 355 360 365	1104
ggc aac atc act agt ggc acc atc acc ctg ccc tgc cgc atc aag cag Gly Asn Ile Thr Ser Gly Thr Ile Thr Leu Pro Cys Arg Ile Lys Gln 370 375 380	1152
atc atc aac atg tgg cag gag gtg ggc aag gcc atg tac gcc ccc ccc Ile Ile Asn Met Trp Gln Glu Val Gly Cys Ala Met Tyr Ala Pro Pro 385 390 395 400	1200
atc ggc ggc cag atc aag tgc ctg agc aac atc acc ggc ctg ctg ctg Ile Gly Gly Gln Ile Lys Cys Leu Ser Asn Ile Thr Gly Leu Leu Leu 405 410 415	1248
acc cgc gac ggc ggc agc gac aac tgc agc agc ggc aag gag att ttc Thr Arg Asp Gly Gly Ser Asp Asn Ser Ser Ser Gly Lys Glu Ile Phe 420 425 430	1296
cgc ccc ggc ggc ggc gac atg cgc gac aac tgg cgc agc gag ctg tac Arg Pro Gly Gly Gly Asp Met Arg Asp Asn Trp Arg Ser Glu Leu Tyr 435 440 445	1344
aag tac aag gtg gtg aag atc gag ccc ctg ggc atc gcc ccc acc aag Lys Tyr Lys Val Val Lys Ile Glu Pro Leu Gly Ile Ala Pro Thr Lys 450 455 460	1392
gcc aag cgc cgc gtg gtg cag cgc gag aag gcc gcc gtg ggc atc gcc Ala Lys Arg Arg Val Val Gln Arg Glu Lys Arg Ala Val Gly Ile Gly 465 470 475 480	1440

gct atg ttc ctc ggc ttc ctg ggc gct gca ggc agc acc atg ggc gcc 1488
 Ala Met Phe Leu Gly Phe Leu Gly Ala Ala Gly Ser Thr Met Gly Ala
 485 490 495
 gcc agc ctg acc ctg acc gtg cag gcc cgc cag ctg ctg agc ggc atc 1536
 Ala Ser Leu Thr Leu Thr Val Gln Ala Arg Gln Leu Leu Ser Gly Ile
 500 505 510
 gtg cag cag cag aac aac ctg ctg cgc gcc atc gag gcc cag cag cac 1584
 Val Gln Gln Gln Asn Asn Leu Leu Arg Ala Ile Glu Ala Gln Gln His
 515 520 525
 ctg ctc cag ctg acc gtg tgg ggc atc aag cag ctc cag gcc cgc gtg 1632
 Leu Leu Gln Leu Thr Val Trp Gly Ile Lys Gln Leu Gln Ala Arg Val
 530 535 540
 ctg gct cta gag cgc tac ctc cag gac cag cgc ttc ctg ggc atg tgg 1680
 Leu Ala Leu Gln Arg Tyr Leu Gln Asp Gln Arg Phe Leu Gly Met Trp
 545 550 555 560
 gcc tgc tcc gcc aag ctg atc tgc acc acg gcc gtg ccc tgg aac gcc 1728
 Gly Cys Ser Gly Lys Leu Ile Cys Thr Thr Ala Val Pro Trp Asn Ala
 565 570 575
 agc tgg agc aac aag aac ctg agc cag att tgg gac aac atg acc tgg 1776
 Ser Trp Ser Asn Lys Asn Leu Ser Gln Ile Trp Asp Asn Met Thr Trp
 580 585 590
 atg gac tgg gag cgc gag atc agc aac tac acc gag atc atc tac agc 1824
 Met Glu Trp Glu Arg Glu Ile Ser Asn Tyr Thr Glu Ile Ile Tyr Ser
 595 600 605
 ctg atc gag gag agc cag aac cag cag gag aag aac gag ctg gac ctg 1872
 Leu Ile Gln Glu Ser Gln Asn Gln Gln Glu Lys Asn Glu Leu Asp Leu
 610 615 620
 ctc cag ctg gac aag tgg gca agc ttg tgt gac tga ttg agg atc c 1918
 Leu Gln Leu Asp Lys Trp Ala Ser Leu Cys Asp * Leu Arg Ile
 625 630 635

*210- 68

*211- 638

*212- 9RT

*213- Artificial Sequence

*400- 68

Ala Ser Ala Ala Asp Arg Leu Trp Val Thr Val Tyr Tyr Gly Val Pro
 1 5 10 15
 Val Trp Lys Asp Ala Thr Thr Thr Leu Phe Cys Ala Ser Asp Ala Lys
 20 25 30
 Ala Tyr Asp Thr Glu Val His Asn Val Trp Ala Thr His Ala Cys Val
 35 40 45
 Pro Thr Asp Pro Asn Pro Gln Glu Val Val Leu Gly Asn Val Thr Glu
 50 55 60
 Asn Phe Asn Met Gly Lys Asn Asn Met Val Glu Gln Met His Glu Asp
 65 70 75 80
 Ile Ile Ser Leu Trp Asp Gln Ser Leu Lys Pro Cys Val Lys Leu Thr

85										90					95				
Pro	Leu	Cys	Val	Thr	Leu	Asn	Cys	Thr	Lys	Leu	Lys	Asn	Ser	Thr	Asp				
Thr	Asn	Asp	Thr	Arg	Trp	Gly	Thr	Gln	Glu	Met	Lys	Asn	Cys	Ser	Phe				
Asn	Ile	Ser	Thr	Ser	Val	Arg	Asn	Lys	Met	Lys	Arg	Glu	Tyr	Ala	Leu				
Phe	Tyr	Ser	Leu	Asp	Ile	Val	Pro	Ile	Asp	Asn	Asp	Asn	Thr	Ser	Tyr				
Arg	Leu	Arg	Ser	Cys	Asn	Thr	Ser	Ile	Ile	Thr	Gln	Ala	Cys	Pro	Lys				
Val	Ser	Phe	Glu	Pro	Ile	Pro	Ile	His	Phe	Cys	Ala	Pro	Ala	Gly	Phe				
Ala	Ile	Leu	Lys	Cys	Asn	Asn	Lys	Thr	Phe	Asn	Gly	Thr	Gly	Pro	Cys				
Thr	Asn	Val	Ser	Thr	Val	Gln	Cys	Thr	His	Gly	Ile	Arg	Pro	Val	Val				
Ser	Thr	Gln	Leu	Leu	Leu	Asn	Gly	Ser	Leu	Ala	Gln	Glu	Glu	Val	Val				
Ile	Arg	Ser	Glu	Asn	Phe	Thr	Asn	Asn	Ala	Lys	Thr	Ile	Ile	Val	Gln				
Leu	Asn	Glu	Ser	Val	Glu	Ile	Asn	Cys	Thr	Arg	Pro	Asn	Asn	Asn	Thr				
Arg	Lys	Ser	Ile	His	Ile	Gly	Pro	Gly	Arg	Ala	Phe	Tyr	Thr	Thr	Gly				
Asp	Ile	Ile	Gly	Asp	Ile	Arg	Gln	Ala	His	Cys	Asn	Ile	Ser	Arg	Thr				
Asn	Trp	Thr	Asn	Thr	Leu	Lys	Arg	Val	Ala	Glu	Lys	Leu	Arg	Glu	Lys				
Phe	Asn	Asn	Thr	Thr	Ile	Val	Phe	Asn	Gln	Ser	Ser	Gly	Gly	Asp	Pro				
Glu	Ile	Val	Met	His	Ser	Phe	Asn	Cys	Gly	Gly	Gln	Phe	Phe	Tyr	Cys				
Asn	Thr	Thr	Gln	Leu	Phe	Asn	Ser	Thr	Trp	Asn	Glu	Thr	Asn	Ser	Glu				
Gly	Asn	Ile	Thr	Ser	Gly	Thr	Ile	Thr	Leu	Pro	Cys	Arg	Ile	Lys	Gln				
Ile	Ile	Asn	Met	Trp	Gln	Glu	Val	Gly	Lys	Ala	Met	Tyr	Ala	Pro	Pro				
Ile	Gly	Gly	Gln	Ile	Lys	Cys	Leu	Ser	Asn	Ile	Thr	Gly	Leu	Leu	Leu				
Thr	Arg	Asp	Gly	Gly	Ser	Asp	Asn	Ser	Ser	Ser	Gly	Lys	Glu	Ile	Phe				
Arg	Pro	Gly	Gly	Gly	Asp	Met	Arg	Asp	Asn	Trp	Arg	Ser	Glu	Leu	Tyr				
Lys	Tyr	Lys	Val	Val	Lys	Ile	Glu	Pro	Leu	Gly	Ile	Ala	Pro	Thr	Lys				
Ala	Lys	Arg	Arg	Val	Val	Gln	Arg	Gln	Lys	Arg	Ala	Val	Gly	Ile	Gly				
Ala	Met	Phe	Leu	Gly	Phe	Leu	Gly	Ala	Ala	Gly	Ser	Thr	Met	Gly	Ala				
Ala	Ser	Leu	Thr	Leu	Thr	Val	Gln	Ala	Arg	Gln	Leu	Leu	Ser	Gly	Ile				
Val	Gln	Gln	Gln	Asn	Asn	Leu	Leu	Arg	Ala	Ile	Glu	Ala	Gln	Gln	His				
Leu	Leu	Gln	Leu	Thr	Val	Trp	Gly	Ile	Lys	Gln	Leu	Gln	Ala	Arg	Val				
Leu	Ala	Leu	Glu	Arg	Tyr	Leu	Gln	Asp	Gln	Arg	Phe	Leu	Gly	Met	Trp				

Gly	Cys	Ser	Gly	Lys	Leu	Ile	Cys	Thr	Thr	Ala	Val	Pro	Trp	Asn	Ala
				565					570					575	
Ser	Trp	Ser	Asn	Lys	Asn	Leu	Ser	Gln	Ile	Trp	Asp	Asn	Met	Thr	Trp
				580				585					590		
Met	Glu	Trp	Glu	Arg	Glu	Ile	Ser	Asn	Tyr	Thr	Glu	Ile	Ile	Tyr	Ser
				595			600					605			
Leu	Ile	Glu	Glu	Ser	Gln	Asn	Gln	Gln	Glu	Lys	Asn	Glu	Leu	Asp	Leu
	610					615					620				
Leu	Gln	Leu	Asp	Lys	Trp	Ala	Ser	Leu	Cys	Asp	Leu	Arg	Ile		
625					630					635					

<210> 69
<211> 2071
<212> DNA
<213> Artificial Sequence

(220)
 (210) CDS
 (220) (1) ... (2071)

44002 69

get agc ggc gcc gac cgc ctg tgg gtg acc gtg tac tac ggc gtg ccc 48
Ala Ser Ala Ala Asp Arg Leu Trp Val Thr Val Tyr Tyr Gly Val Pro
1 5 10 15

gtg tgg aag gac gcc acc acc acc ctg ttc tgc gcc agc gac gcc aag 96
Val Trp Lys Asp Ala Thr Thr Thr Leu Phe Cys Ala Ser Asp Ala Lys
20 25 30

gcc tac aac acc gag gtg cac aac gtg tgg gcc acc cac gcg tgc gtg 144
Ala Tyr Asp Thr Glu Val His Asn Val Trp Ala Thr His Ala Cys Val
35 40 45

ccg acc gac ccc aac ccc cag gag gtg gtg ctg ggc aac gtg acc gag 192
Pro Thr Asp Pro Asn Pro Gln Glu Val Val Leu Gly Asn Val Thr Glu
50 55 60

aac ttc aac atg ggc aag aac aac atg gtg gag gag atg cac gag gat 240
Asn Phe Asn Met Gly Lys Asn Asn Met Val Glu Gln Met His Glu Asp
65 70 75 80

atc atc aqc ctg tgg gac cag agc ctg aag ccc tgc gtg aag ctg acc 288
Ile Ile Ser Leu Trp Asp Gln Ser Leu Lys Pro Cys Val Lys Leu Thr
35 90 95

acc ctg tgc gtg acc ctg aac tgc acc aag ctg aag aac agc acc gac 336
Pro Leu Cys Val Thr Leu Asn Cys Thr Lys Leu Lys Asn Ser Thr Asp
100 105 110

acc aac aac acc cgc tgg ggc acc cag gag atg aag aac tgc agc ttc 364
Thr Asn Asn Thr Arg Trp Gly Thr Gln Glu Met Lys Asn Cys Ser Phe
115 120 125

aac att ago aas ago gtg cgc aac aag atg aag cgc gag tac gcc ctg 402
 Asn Ile Ser Thr Ser Val Arg Asn Lys Met Lys Arg Glu Tyr Ala Leu
 130 135 140

ttc tac agc ctg gac atc gtg ccc atc gac aac gac aac acc agc tac
 Phe Tyr Ser Leu Asp Ile Val Pro Ile Asp Asn Asp Asn Thr Ser Tyr

145	150	155	160	
cgc ctg cgc agc tgc aac aca tgc atc atc acc cag gcc tgc ccc aag				528
Arg Leu Arg Ser Cys Asn Thr Ser Ile Ile Thr Gln Ala Cys Pro Lys				
	165	170	175	
gtg agc ttc gag ccc atc ccc atc cac ttc tgc gcc ccc gcc ggc ttc				576
Val Ser Phe Glu Pro Ile Pro Ile His Phe Cys Ala Pro Ala Gly Phe				
	180	185	190	
gcc atc ctg aag tgc aac aac aag acc ttc aac ggc acc gcc ccc tgc				624
Ala Ile Leu Lys Cys Asn Asn Lys Thr Phe Asn Gly Thr Gly Pro Cys				
	195	200	205	
acc aac gtg agc acc gtg cag tgc acc cac gga att cgc ccc gtg gtg				672
Thr Asn Val Ser Thr Val Gln Cys Thr His Gly Ile Arg Pro Val Val				
	210	215	220	
agc acc cag ctg ctg ctg aac ggc agc ctg gcc gag gag gag gtg gtg				720
Ser Thr Gln Leu Leu Leu Asn Gly Ser Leu Ala Glu Glu Glu Val Val				
	225	230	235	240
atc aga tct gag aac ttc acc aac aac gcc aag acc atc atc gtg cag				768
Ile Arg Ser Glu Asn Phe Thr Asn Asn Ala Lys Thr Ile Ile Val Gln				
	245	250	255	
ctg aac gag agc gtg gag atc aac tgc acc cgc ccc aac aac aac acc				816
Leu Asn Glu Ser Val Glu Ile Asn Cys Thr Arg Pro Asn Asn Asn Thr				
	260	265	270	
cgc aag agc atc cac atc ggc cct ggc cgc gcc ttc tac acc acc gcc				864
Arg Lys Ser Ile His Ile Gly Pro Gly Arg Ala Phe Tyr Thr Thr Gly				
	275	280	285	
gac atc atc gcc gac atc cgc cag gcc cac tgc aac atc tct aga acc				912
Asp Ile Ile Gly Asp Ile Arg Gln Ala His Cys Asn Ile Ser Arg Thr				
	290	295	300	
aac tgg acc aac acc ctg aag cgc gtg gcc gag aag ctg cgc gag aag				960
Asn Trp Thr Asn Thr Leu Lys Arg Val Ala Glu Lys Leu Arg Glu Lys				
	305	310	315	320
ttc aac aac acc acc atc gtg ttc aac cag agc tcc gcc gcc gac ccc				1008
Phe Asn Asn Thr Thr Ile Val Phe Asn Gln Ser Ser Gly Gly Asp Pro				
	325	330	335	
gag atc gtg atg cac agc ttc aac tgc gcc gcc gag ttc ttc tac tgc				1056
Glu Ile Val Met His Ser Phe Asn Cys Gly Gly Glu Phe Phe Tyr Cys				
	340	345	350	
aac acc acc cag ctg ttc aac agc acc tgg aac gag acc aac agc gag				1104
Asn Thr Thr Gln Leu Phe Asn Ser Thr Trp Asn Glu Thr Asn Ser Glu				
	355	360	365	
ggc aac atc act agt gcc acc atc acc ctg ccc tgc cgc atc aag cag				
Gly Asn Ile Thr Ser Gly Thr Ile Thr Leu Pro Cys Arg Ile Lys Gln				
	370	375	380	
atc atc aac atg tgg cag gag gtg gcc aag gcc atc tac gcc ccc ccc				

Ile Ile Asn Met Trp Gln Glu Val Gly Lys Ala Met Tyr Ala Pro Pro	
385 390 395 400	
atc ggc ggc cag atc aag tgc ctg agc aac atc acc ggc ctg ctg ctg	1248
Ile Gly Gly Gln Ile Lys Cys Leu Ser Asn Ile Thr Gly Leu Leu Leu	
405 410 415	
acc cgc gac ggc ggc agc gac aac tgc agc agc ggc aag gag att ttc	1296
Thr Arg Asp Gly Gly Ser Asp Asn Ser Ser Ser Gly Lys Glu Ile Phe	
420 425 430	
cgc ccc ggc ggc ggc gac atg cgc gac aac tgg cgc agc gag ctg tac	1344
Arg Pro Gly Gly Gly Asp Met Arg Asp Asn Trp Arg Ser Glu Leu Tyr	
435 440 445	
aag tac aag gtg gtg aag atc gag ccc ctg ggc atc gcc ccc acc aag	1392
Lys Tyr Lys Val Val Lys Ile Glu Pro Leu Gly Ile Ala Pro Thr Lys	
450 455 460	
gcc aag cgc cgc gtg gtg cag cgc gag aag cgc gcc gtg ggc atc ggc	1440
Ala Lys Arg Arg Val Val Gln Arg Glu Lys Arg Ala Val Gly Ile Gly	
465 470 475 480	
gct atg ttc ctc ggc ttc ctg ggc gct gca ggc agc acc atg ggc gcc	1488
Ala Met Phe Leu Gly Phe Leu Gly Ala Ala Gly Ser Thr Met Gly Ala	
485 490 495	
gcc agc ctg acc ctg acc gtg cag gcc cgc cag ctg ctg agc ggc atc	1536
Ala Ser Leu Thr Leu Thr Val Gln Ala Arg Gln Leu Leu Ser Gly Ile	
500 505 510	
gtg cag cag cag aac aac ctg ctg cgc gcc atc gag gcc cag cag cag	1584
Val Gln Gln Gln Asn Asn Leu Leu Arg Ala Ile Glu Ala Gln Gln His	
515 520 525	
ctg ctc cag ctg acc gtg tgg ggc atc aag cag ctc cag gcc cgc gtg	1632
Leu Leu Gln Leu Thr Val Trp Gly Ile Lys Gln Leu Gln Ala Arg Val	
530 535 540	
ctg gct cta gag cgc tac ctc cag gac cag cgc ttc ctg gcc atg tgg	1680
Leu Ala Leu Glu Arg Tyr Leu Gln Asp Gln Arg Phe Leu Gly Met Trp	
545 550 555 560	
ggc tgc tcc ggc aag ctg atc tgc acc acg gcc gtg ccc tgg aac gcc	1728
Gly Cys Ser Gly Lys Leu Ile Cys Thr Thr Ala Val Pro Trp Asn Ala	
565 570 575	
agc tgg agc aac aag aac ctg agc cag att tgg gac aac atg acc tgg	1776
Ser Trp Ser Asn Lys Asn Leu Ser Gln Ile Trp Asp Asn Met Thr Trp	
580 585 590	
atg gac tga gag cgc gag atc agc aac tac acc gag atc atc tac agc	1824
Met Glu Trp Glu Arg Glu Ile Ser Asn Tyr Thr Gln Ile Ile Tyr Ser	
595 600 605	
ctg atc gag gag agc cag aac cag cag gag aag aac gag ctg gac ctg	
Leu Ile Glu Glu Ser Gln Asn Gln Gln Gln Lys Asn Glu Leu Asp Leu	
610 615 620	

ctc cag ctg gac aag tgg gca agc ttg tgg aac tgg ttc aac atc acc 1920
 Leu Gln Leu Asp Lys Trp Ala Ser Leu Trp Asn Trp Phe Asn Ile Thr
 625 630 635 640
 aac tgg ctg tgg tac atc aag att ttc atc atg atc gtg ggc ggc ctg 1968
 Asn Trp Leu Trp Tyr Ile Lys Ile Phe Ile Met Ile Val Gly Gly Leu
 645 650 655
 atc ggc ctg cgc atc gtg ttc acc gtg ctg agc atc gtg aac cgc gtg 2016
 Ile Gly Leu Arg Ile Val Phe Thr Val Leu Ser Ile Val Asn Arg Val
 660 665 670
 cgc cag gga tgc agc ccc ctg agc ttc cag acc cgc ctg ccc gtg tga 2064
 Arg Gln Gly Cys Ser Pro Leu Ser Phe Gln Thr Arg Leu Pro Val *
 675 680 685
 cgg atc c 2071
 Arg Ile

210: 70
 211: 689
 212: PRT
 213: Artificial Sequence

400: 70
 Ala Ser Ala Ala Asp Arg Leu Trp Val Thr Val Tyr Tyr Gly Val Pro
 1 5 10 15
 Val Trp Lys Asp Ala Thr Thr Thr Leu Phe Cys Ala Ser Asp Ala Lys
 20 25 30
 Ala Tyr Asp Thr Glu Val His Asn Val Trp Ala Thr His Ala Cys Val
 35 40 45
 Pro Thr Asp Pro Asn Pro Gln Glu Val Val Leu Gly Asn Val Thr Glu
 50 55 60
 Asn Phe Asn Met Gly Lys Asn Asn Met Val Glu Gln Met His Glu Asp
 65 70 75 80
 Ile Ile Ser Leu Trp Asp Gln Ser Leu Lys Pro Cys Val Lys Leu Thr
 85 90 95
 Pro Leu Cys Val Thr Leu Asn Cys Thr Lys Leu Lys Asn Ser Thr Asp
 100 105 110
 Thr Asn Asn Thr Arg Trp Gly Thr Gln Glu Met Lys Asn Cys Ser Phe
 115 120 125
 Asn Ile Ser Thr Ser Val Arg Asn Lys Met Lys Arg Glu Tyr Ala Leu
 130 135 140
 Phe Tyr Ser Leu Asp Ile Val Pro Ile Asp Asn Asp Asn Thr Ser Tyr
 145 150 155 160
 Arg Leu Arg Ser Cys Asn Thr Ser Ile Ile Thr Gln Ala Cys Pro Lys
 165 170 175
 Val Ser Phe Glu Pro Ile Pro Ile His Phe Cys Ala Pro Ala Gly Phe
 180 185 190
 Ala Ile Leu Lys Cys Asn Asn Lys Thr Phe Asn Gly Thr Gly Pro Cys
 195 200 205
 Thr Asn Val Ser Thr Val Gln Cys Thr His Gly Ile Arg Pro Val Val
 210 215 220
 Ser Thr Gln Leu Leu Leu Asn Gly Ser Leu Ala Glu Glu Glu Val Val
 225 230 235 240
 Ile Arg Ser Gln Asn Phe Thr Asn Asn Ala Lys Thr Ile Ile Val Gln
 245 250 255

Leu Asn Glu Ser Val Glu Ile Asn Cys Thr Arg Pro Asn Asn Asn Thr
 260 265 270
 Arg Lys Ser Ile His Ile Gly Pro Gly Arg Ala Phe Tyr Thr Thr Gly
 275 280 285
 Asp Ile Ile Gly Asp Ile Arg Gln Ala His Cys Asn Ile Ser Arg Thr
 290 295 300
 Asn Trp Thr Asn Thr Leu Lys Arg Val Ala Glu Lys Leu Arg Glu Lys
 305 310 315 320
 Phe Asn Asn Thr Thr Ile Val Phe Asn Gln Ser Ser Gly Gly Asp Pro
 325 330 335
 Glu Ile Val Met His Ser Phe Asn Cys Gly Gly Glu Phe Phe Tyr Cys
 340 345 350
 Asn Thr Thr Gln Leu Phe Asn Ser Thr Trp Asn Glu Thr Asn Ser Glu
 355 360 365
 Gly Asn Ile Thr Ser Gly Thr Ile Thr Leu Pro Cys Arg Ile Lys Gln
 370 375 380
 Ile Ile Asn Met Trp Gln Glu Val Gly Lys Ala Met Tyr Ala Pro Pro
 385 390 395 400
 Ile Gly Gly Gln Ile Lys Cys Leu Ser Asn Ile Thr Gly Leu Leu Leu
 405 410 415
 Thr Arg Asp Gly Gly Ser Asp Asn Ser Ser Ser Gly Lys Glu Ile Phe
 420 425 430
 Arg Pro Gly Gly Gly Asp Met Arg Asp Asn Trp Arg Ser Glu Leu Tyr
 435 440 445
 Lys Tyr Lys Val Val Lys Ile Glu Pro Leu Gly Ile Ala Pro Thr Lys
 450 455 460
 Ala Lys Arg Arg Val Val Gln Arg Glu Lys Arg Ala Val Gly Ile Gly
 465 470 475 480
 Ala Met Phe Leu Gly Phe Leu Gly Ala Ala Gly Ser Thr Met Gly Ala
 485 490 495
 Ala Ser Leu Thr Leu Thr Val Gln Ala Arg Gln Leu Leu Ser Gly Ile
 500 505 510
 Val Gln Gln Gln Asn Asn Leu Leu Arg Ala Ile Glu Ala Gln Gln His
 515 520 525
 Leu Leu Gln Leu Thr Val Trp Gly Ile Lys Gln Leu Gln Ala Arg Val
 530 535 540
 Leu Ala Leu Glu Arg Tyr Leu Gln Asp Gln Arg Phe Leu Gly Met Trp
 545 550 555 560
 Gly Cys Ser Gly Lys Leu Ile Cys Thr Thr Ala Val Pro Trp Asn Ala
 565 570 575
 Ser Trp Ser Asn Lys Asn Leu Ser Gln Ile Trp Asp Asn Met Thr Trp
 580 585 590
 Met Glu Trp Glu Arg Glu Ile Ser Asn Tyr Thr Glu Ile Ile Tyr Ser
 595 600 605
 Leu Ile Glu Glu Ser Gln Asn Gln Gln Glu Lys Asn Glu Leu Asp Leu
 610 615 620
 Leu Gln Leu Asp Lys Trp Ala Ser Leu Trp Asn Trp Phe Asn Ile Thr
 625 630 635 640
 Asn Trp Leu Trp Tyr Ile Lys Ile Phe Ile Met Ile Val Gly Gly Leu
 645 650 655
 Ile Gly Leu Arg Ile Val Phe Thr Val Leu Ser Ile Val Asn Arg Val
 660 665 670
 Arg Gln Gly Cys Ser Pro Leu Ser Phe Gln Thr Arg Leu Pro Val Arg
 675 680 685
 Ile

<210> 71

<211> 2469

<212> DNA

<213> Artificial Sequence

<220>

<221> CDS

<222> (1)...(2469)

<400> 71

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 Ala Ser Ala Ala Asp Arg Leu Trp Val Thr Val Tyr Tyr Gly Val Pro
 1 5 10 15

ggg tgg aag gac gcc acc acc acc ctg ttc tgc gcc agc gac gcc aag 96
 Val Trp Lys Asp Ala Thr Thr Thr Leu Phe Cys Ala Ser Asp Ala Lys
 20 25 30

gcc tac gac acc gag gtg cac aac gtg tgg gcc acc cac gcc tgc gtg 144
 Ala Tyr Asp Thr Glu Val His Asn Val Trp Ala Thr His Ala Cys Val
 35 40 45

ccc acc gac ccc aac ccc cag gag gtg gtg ctg ggc aac gtg acc gag 192
 Pro Thr Asp Pro Asn Pro Gln Glu Val Val Leu Gly Asn Val Thr Glu
 50 55 60

aac ttc aac atg ggc aag aac aac atg gtg gag cag atg cac gag gat 240
 Asn Phe Asn Met Gly Lys Asn Asn Met Val Glu Gln Met His Glu Asp
 65 70 75 80

atc atc agc ctg tgg gac cag agc ctg aag ccc tgc gtg aag ctg acc 288
 Ile Ile Ser Leu Trp Asp Gln Ser Leu Lys Pro Cys Val Lys Leu Thr
 85 90 95

ccc ctg tgc gtg acc ctg aac tgc acc aag ctg aag aac agc acc gac 336
 Pro Leu Cys Val Thr Leu Asn Cys Thr Lys Leu Lys Asn Ser Thr Asp
 100 105 110

acc aac aac acc cgc tgg gcc acc cag gag atg aag aac tgc agc ttc 384
 Thr Asn Asn Thr Arg Trp Gly Thr Gln Glu Met Lys Asn Cys Ser Phe
 115 120 125

aac atc agc acc agc gtg cgc aac aag atg aag cgc gag tac gcc ctg 432
 Asn Ile Ser Thr Ser Val Arg Asn Lys Met Lys Arg Glu Tyr Ala Leu
 130 135 140

ttc tac agc ctg gac atc gtg ccc atc gac aac gac aac acc agc tac 480
 Phe Tyr Ser Leu Asp Ile Val Pro Ile Asp Asn Asp Asn Thr Ser Tyr
 145 150 155 160

cgc ctg cgc agc tgc aac aca tgc atc atc acc cag gcc tgc ccc aag 528
 Arg Leu Arg Ser Cys Asn Thr Ser Ile Ile Thr Gln Ala Cys Pro Lys
 165 170 175

gtg agc ttc gag ccc atc ccc atc cac ttc tgc gcc ccc gcc gcc ttc 576
 Val Ser Phe Glu Pro Ile Pro Ile His Phe Cys Ala Pro Ala Gly Phe
 180 185 190

gcc atc ctg aag tgc aac aac aag acc ttc aac gcc acc gcc ccc tgc 624
 Ala Ile Leu Lys Cys Asn Asn Lys Thr Phe Asn Gly Thr Gly Pro Cys
 195 200 205

acc aac gtg agc acc gtg cag tgc acc cac gga att cgc ccc gtg gtg	672
Thr Asn Val Ser Thr Val Gln Cys Thr His Gly Ile Arg Pro Val Val	
210 215 220	
agc acc cag ctg ctg ctg aac ggc agc ctg gcc gag gag gag gtg gtg	720
Ser Thr Gln Leu Leu Leu Asn Gly Ser Leu Ala Glu Glu Glu Val Val	
225 230 235 240	
atc aga tct gag aac ttc acc aac aac gcc aag acc atc atc gtg cag	768
Ile Arg Ser Glu Asn Phe Thr Asn Asn Ala Lys Thr Ile Ile Val Gln	
245 250 255	
ctg aac gag agc gtg gag atc aac tgc acc gcc ccc aac aac aac acc	816
Leu Asn Glu Ser Val Glu Ile Asn Cys Thr Arg Pro Asn Asn Asn Thr	
260 265 270	
cgc aag agc atc cac atc ggc cct gcc gcc gcc ttc tac acc acc gcc	864
Arg Lys Ser Ile His Ile Gly Pro Gly Arg Ala Phe Tyr Thr Thr Gly	
275 280 285	
gac atc atc gcc gac atc cgc cag gcc cac tgc aac atc tct aga acc	912
Asp Ile Ile Gly Asp Ile Arg Gln Ala His Cys Asn Ile Ser Arg Thr	
290 295 300	
aac tgg acc aac acc ctg aag gcc gtg gcc gag aag ctg cgc gag aag	960
Asn Trp Thr Asn Thr Leu Lys Arg Val Ala Glu Lys Leu Arg Glu Lys	
305 310 315 320	
ttc aac aac acc acc atc gtg ttc aac cag agc tcc gcc gcc gac ccc	1008
Phe Asn Asn Thr Thr Ile Val Phe Asn Gln Ser Ser Gly Gly Asp Pro	
325 330 335	
gag atc gtg atg cac agc ttc aac tgc gcc gcc gag ttc ttc tac tgc	1056
Glu Ile Val Met His Ser Phe Asn Cys Gly Gly Glu Phe Phe Tyr Cys	
340 345 350	
aac acc acc cag ctg ttc aac agc acc tgg aac gag acc aac agc gag	1104
Asn Thr Thr Gln Leu Phe Asn Ser Thr Trp Asn Glu Thr Asn Ser Glu	
355 360 365	
ggc aac atc act agt gcc acc atc acc ctg ccc tgc gcc atc aag cag	1152
Gly Asn Ile Thr Ser Gly Thr Ile Thr Leu Pro Cys Arg Ile Lys Gln	
370 375 380	
atc atc aac atg tgg cag gag gtg gcc aag gcc atg tac gcc ccc ccc	1200
Ile Ile Asn Met Trp Gln Glu Val Gly Lys Ala Met Tyr Ala Pro Pro	
385 390 395 400	
atc gcc gcc cag atc aag tgc ctg agc aac atc acc gcc ctg ctg ctg	1248
Ile Gly Gly Gln Ile Lys Cys Leu Ser Asn Ile Thr Gly Leu Leu Leu	
405 410 415	
acc gcc gac gcc gcc agc gac aac tgc agc agc gcc aag gag att ttc	1296
Thr Arg Asp Gly Ser Asp Asn Ser Ser Ser Gly Lys Glu Ile Phe	
420 425 430	
cgc ccc gcc gcc gcc gac atg cgc gac aac tgg cgc agc gag ctg tac	1344
Arg Pro Gly Gly Gly Asp Met Arg Asp Asn Trp Arg Ser Glu Leu Tyr	

435	440	445	
aag tac aag gtg gtg aag atc gag ccc ctg ggc atc gcc ccc acc aag Lys Tyr Lys Val Val Lys Ile Glu Pro Leu Gly Ile Ala Pro Thr Lys 450 455 460			1392
gcc aag cgc cgc gtg gtg cag cgc gag aag cgc gcc gtg ggc atc ggc Ala Lys Arg Arg Val Val Gln Arg Glu Lys Arg Ala Val Gly Ile Gly 465 470 475 480			1440
gct atg ttc ctc ggc ttc ctg ggc gct gca ggc agc acc atg ggc gcc Ala Met Phe Leu Gly Phe Leu Gly Ala Ala Gly Ser Thr Met Gly Ala 485 490 495			1488
gcc agc ctg acc ctg acc gtg cag gcc cgc cag ctg ctg agc ggc atc Ala Ser Leu Thr Leu Thr Val Gln Ala Arg Gln Leu Leu Ser Gly Ile 500 505 510			1536
gtg cag cag cag aac aac ctg ctg cgc gcc atc gag gcc cag cag cac Val Gln Gln Gln Asn Asn Leu Leu Arg Ala Ile Glu Ala Gln Gln His 515 520 525			1584
ctg ctc cag ctg acc gtg tgg ggc atc aag cag ctc cag gcc cgc gtg Leu Leu Gln Leu Thr Val Trp Gly Ile Lys Gln Leu Gln Ala Arg Val 530 535 540			1632
ctg gct cta gag cgc tac ctc cag gac cag cgc ttc ctg ggc atg tgg Leu Ala Leu Glu Arg Tyr Leu Gln Asp Gln Arg Phe Leu Gly Met Trp 545 550 555 560			1680
ggc tgc tcc ggc aag ctg atc tgc acc acg gcc gtg ccc tgg aac gcc Gly Cys Ser Gly Lys Leu Ile Cys Thr Thr Ala Val Pro Trp Asn Ala 565 570 575			1728
agc tgg agc aac aag aac ctg agc cag att tgg gac aac atg acc tgg Ser Trp Ser Asn Lys Asn Leu Ser Gln Ile Trp Asp Asn Met Thr Trp 580 585 590			1776
atg gag tgg gag cgc gag atc agc aac tac acc gag atc atc tac agc Met Glu Trp Glu Arg Glu Ile Ser Asn Tyr Thr Glu Ile Ile Tyr Ser 595 600 605			1824
ctg atc gag gag agc cag aac cag cag gag aag aac gag ctg gac ctg Leu Ile Glu Glu Ser Gln Asn Gln Gln Glu Lys Asn Glu Leu Asp Leu 610 615 620			1872
ctc cag ctg gac aag tgg gca agc ttg tga aac tgg ttc aac atc acc Leu Gln Leu Asp Lys Trp Ala Ser Leu Trp Asn Trp Phe Asn Ile Thr 625 630 635 640			1920
aac tgg ctg tgg tac atc aag att ttc atc atg atc gtg ggc ggc ctg Asn Trp Leu Trp Tyr Ile Lys Ile Phe Ile Met Ile Val Gly Gly Leu 645 650 655			1968
atc gcc ctg cgc atc gtg ttc acc gtg ctg agc atc gtg aac cgc gtg Ile Gly Leu Arg Ile Val Phe Thr Val Leu Ser Ile Val Asn Arg Val 660 665 670			2016
cgc cag gac tac aac ccc ctg agc ttc cag acc cgc ctg ccc gtg ccc			2064

Arg Gln Gly Tyr Ser Pro Leu Ser Phe Gln Thr Arg Leu Pro Val Pro
 675 680 685
 cgc ggc ccc gac cgc ccc gag ggc atc gag gag gag ggc ggc gag cgc 2112
 Arg Gly Pro Asp Arg Pro Glu Gly Ile Glu Glu Glu Gly Gly Glu Arg
 690 695 700
 gac cgc gac cgc agc acc cgc ctg gtg acc ggc ttc ctg ccc ctg atc 2160
 Asp Arg Asp Arg Ser Thr Arg Leu Val Thr Gly Phe Leu Pro Leu Ile
 705 710 715 720
 tgg gac gac ctg cgc agc ctg ttc ctg ttc agc tac cat cga ttg cgc 2208
 Trp Asp Asp Leu Arg Ser Leu Phe Leu Phe Ser Tyr His Arg Leu Arg
 725 730 735
 gac ctg ctg ctg atc gtg gcc cgc atc gtg gag ctg ctg ggc cgc cgc 2256
 Asp Leu Leu Leu Ile Val Ala Arg Ile Val Glu Leu Leu Gly Arg Arg
 740 745 750
 ggc tgg gag atc ctg aag tac tgg tgg aac ctg ctc cag tac tgg agc 2304
 Gly Trp Glu Ile Leu Lys Tyr Trp Trp Asn Leu Leu Gln Tyr Trp Ser
 755 760 765
 cag gag ctg aag aac tct gca gtg agc ctg ctg aac gcc acc gcc atc 2352
 Gln Glu Leu Lys Asn Ser Ala Val Ser Leu Leu Asn Ala Thr Ala Ile
 770 775 780
 gcc gtg gcc gag gcc acc gac cgc gtg atc gag gtg gtg cag cgc atc 2400
 Ala Val Ala Glu Gly Thr Asp Arg Val Ile Glu Val Val Gln Arg Ile
 785 790 795 800
 tgg cgc ggc atc ctg cac atc ccc acc cga att cgc cag gcc ttc gag 2448
 Trp Arg Gly Ile Leu His Ile Pro Thr Arg Ile Arg Gln Gly Phe Glu
 805 810 815
 cgc gcc ctg ctg taa gga tcc 2469
 Arg Ala Leu Leu Gly Ser
 820

210 72

211 822

212 PRT

213 Artificial Sequence

400 72

Ala Ser Ala Ala Asp Arg Leu Trp Val Thr Val Tyr Tyr Gly Val Pro
 1 5 10 15
 Val Trp Lys Asp Ala Thr Thr Thr Leu Phe Cys Ala Ser Asp Ala Lys
 20 25 30
 Ala Tyr Asp Thr Glu Val His Asn Val Trp Ala Thr His Ala Cys Val
 35 40 45
 Pro Thr Asp Pro Asn Pro Gln Glu Val Val Leu Gly Asn Val Thr Glu
 50 55 60
 Asn Phe Asn Met Gly Lys Asn Asn Met Val Glu Gln Met His Glu Asp
 65 70 75 80
 Ile Ile Ser Leu Trp Asp Gln Ser Leu Lys Pro Cys Val Lys Leu Thr
 85 90 95
 Pro Leu Cys Val Thr Leu Asn Cys Thr Lys Leu Lys Asn Ser Thr Asp

100							105							110						
Thr	Asn	Asn	Thr	Arg	Trp	Gly	Thr	Gln	Glu	Met	Lys	Asn	Cys	Ser	Phe					
		115						120					125							
Asn	Ile	Ser	Thr	Ser	Val	Arg	Asn	Lys	Met	Lys	Arg	Glu	Tyr	Ala	Leu					
	130					135						140								
Phe	Tyr	Ser	Leu	Asp	Ile	Val	Pro	Ile	Asp	Asn	Asp	Asn	Thr	Ser	Tyr					
	145				150				155						160					
Arg	Leu	Arg	Ser	Cys	Asn	Thr	Ser	Ile	Ile	Thr	Gln	Ala	Cys	Pro	Lys					
				165					170					175						
Val	Ser	Phe	Glu	Pro	Ile	Pro	Ile	His	Phe	Cys	Ala	Pro	Ala	Gly	Phe					
			180					185					190							
Ala	Ile	Leu	Lys	Cys	Asn	Asn	Lys	Thr	Phe	Asn	Gly	Thr	Gly	Pro	Cys					
		195						200					205							
Thr	Asn	Val	Ser	Thr	Val	Gln	Cys	Thr	His	Gly	Ile	Arg	Pro	Val	Val					
	210					215						220								
Ser	Thr	Gln	Leu	Leu	Leu	Asn	Gly	Ser	Leu	Ala	Glu	Glu	Glu	Val	Val					
	225				230					235					240					
Ile	Arg	Ser	Glu	Asn	Phe	Thr	Asn	Asn	Ala	Lys	Thr	Ile	Ile	Val	Gln					
				245					250					255						
Leu	Asn	Glu	Ser	Val	Glu	Ile	Asn	Cys	Thr	Arg	Pro	Asn	Asn	Asn	Thr					
		260						265					270							
Arg	Lys	Ser	Ile	His	Ile	Gly	Pro	Gly	Arg	Ala	Phe	Tyr	Thr	Thr	Gly					
	275					280						285								
Asp	Ile	Ile	Gly	Asp	Ile	Arg	Gln	Ala	His	Cys	Asn	Ile	Ser	Arg	Thr					
	290					295					300									
Asn	Trp	Thr	Asn	Thr	Leu	Lys	Arg	Val	Ala	Glu	Lys	Leu	Arg	Glu	Lys					
	305				310					315					320					
Phe	Asn	Asn	Thr	Thr	Ile	Val	Phe	Asn	Gln	Ser	Ser	Gly	Gly	Asp	Pro					
				325					330					335						
Glu	Ile	Val	Met	His	Ser	Phe	Asn	Cys	Gly	Gly	Glu	Phe	Phe	Tyr	Cys					
		340						345					350							
Asn	Thr	Thr	Gln	Leu	Phe	Asn	Ser	Thr	Trp	Asn	Glu	Thr	Asn	Ser	Glu					
	355							360				365								
Gly	Asn	Ile	Thr	Ser	Gly	Thr	Ile	Thr	Leu	Pro	Cys	Arg	Ile	Lys	Gln					
	370					375					380									
Ile	Ile	Asn	Met	Trp	Gln	Glu	Val	Gly	Lys	Ala	Met	Tyr	Ala	Pro	Pro					
	385				390					395					400					
Ile	Gly	Gly	Gln	Ile	Lys	Cys	Leu	Ser	Asn</											

Ser Trp Ser Asn Lys Asn Leu Ser Gln Ile Trp Asp Asn Met Thr Trp
 580 585 590
 Met Glu Trp Glu Arg Glu Ile Ser Asn Tyr Thr Glu Ile Ile Tyr Ser
 595 600 605
 Leu Ile Glu Glu Ser Gln Asn Gln Gln Glu Lys Asn Glu Leu Asp Leu
 610 615 620
 Leu Gln Leu Asp Lys Trp Ala Ser Leu Trp Asn Trp Phe Asn Ile Thr
 625 630 635 640
 Asn Trp Leu Trp Tyr Ile Lys Ile Phe Ile Met Ile Val Gly Gly Leu
 645 650 655
 Ile Gly Leu Arg Ile Val Phe Thr Val Leu Ser Ile Val Asn Arg Val
 660 665 670
~~Arg~~ Gln Gly Tyr Ser Pro Leu Ser Phe Gln Thr Arg Leu Pro Val Pro
 675 680 685
 Arg Gly Pro Asp Arg Pro Glu Gly Ile Glu Glu Glu Gly Gly Glu Arg
 690 695 700
 Asp Arg Asp Arg Ser Thr Arg Leu Val Thr Gly Phe Leu Pro Leu Ile
 705 710 715 720
 Trp Asp Asp Leu Arg Ser Leu Phe Leu Phe Ser Tyr His Arg Leu Arg
 725 730 735
 Asp Leu Leu Leu Ile Val Ala Arg Ile Val Glu Leu Leu Gly Arg Arg
 740 745 750
 Gly Trp Glu Ile Leu Lys Tyr Trp Trp Asn Leu Leu Gln Tyr Trp Ser
 755 760 765
 Gln Glu Leu Lys Asn Ser Ala Val Ser Leu Leu Asn Ala Thr Ala Ile
 770 775 780
 Ala Val Ala Glu Gly Thr Asp Arg Val Ile Glu Val Val Gln Arg Ile
 785 790 795 800
 Trp Arg Gly Ile Leu His Ile Pro Thr Arg Ile Arg Gln Gly Phe Glu
 805 810 815
 Arg Ala Leu Leu Gly Ser
 820

0210: 73

0211: 1431

0212: CNA

0213: Artificial Sequence

0220:

0221: CDS

0222: (1)...(1431)

0400: 73

gct	agc	gcg	gcc	gac	cgc	ctg	tgg	gtg	acc	gtg	tac	tac	ggc	gtg	ccc	48
Ala	Ser	Ala	Ala	Asp	Arg	Leu	Trp	Val	Thr	Val	Tyr	Tyr	Gly	Val	Pro	
1				5					10					15		
gtg	tgg	aag	gac	gcc	acc	acc	acc	ctg	ttc	tgc	gcc	agc	gac	gcc	aag	96
Val	Trp	Lys	Asp	Ala	Thr	Thr	Thr	Leu	Phe	Cys	Ala	Ser	Asp	Ala	Lys	
				20				25					30			
gcc	tac	gac	acc	gag	gtg	cac	aac	gtg	tgg	gcc	acc	cac	gcg	tgc	gtg	144
Ala	Tyr	Asp	Thr	Glu	Val	His	Asn	Val	Trp	Ala	Thr	His	Ala	Cys	Val	
				35				40					45			
ccc	acc	gac	ccc	aac	ccc	cag	gag	gtg	gtg	ctg	ggc	aac	gtg	acc	gag	192
Pro	Thr	Asp	Pro	Asn	Pro	Gln	Glu	Val	Val	Leu	Gly	Asn	Val	Thr	Glu	
				50			55					60				

aac ttc aac atg ggc aag aac aac atg gtg gag cag atg cac gag gat Asn Phe Asn Met Gly Lys Asn Asn Met Val Glu Gln Met His Glu Asp 65 70 75 80	240
atc atc agc ctg tgg gac cag agc ctg aag ccc tgc gtg aag ctg acc Ile Ile Ser Leu Trp Asp Gln Ser Leu Lys Pro Cys Val Lys Leu Thr 85 90 95	288
ccc ctg tgc gtg acc ctg aac tgc acc aag ctg aag aac agc acc gac Pro Leu Cys Val Thr Leu Asn Cys Thr Lys Leu Lys Asn Ser Thr Asp 100 105 110	336
acc aac aac acc cgc tgg ggc acc cag-gag atg aag aac tgc agc ttc Thr Asn Asn Thr Arg Trp Gly Thr Gln Glu Met Lys Asn Cys Ser Phe 115 120 125	384
aac atc agc acc agc gtg cgc aac aag atg aag cgc gag tac gcc ctg Asn Ile Ser Thr Ser Val Arg Asn Lys Met Lys Arg Glu Tyr Ala Leu 130 135 140	432
ttc tac agc ctg gac atc gtg ccc atc gac aac gag aac acc agc tac Phe Tyr Ser Leu Asp Ile Val Pro Ile Asp Asn Asp Asn Thr Ser Tyr 145 150 155 160	430
cgc ctg cgc agc tgc aac aca tgc atc atc acc cag gcc tgc ccc aag Arg Leu Arg Ser Cys Asn Thr Ser Ile Ile Thr Gln Ala Cys Pro Lys 165 170 175	528
gtg agc ttc gag ccc atc ccc atc cac ttc tgc gcc ccc gcc gcc ttc Val Ser Phe Glu Pro Ile Pro Ile His Phe Cys Ala Pro Ala Gly Phe 180 185 190	576
gcc atc ctg aag tgc aac aac aag acc ttc aac gcc acc gcc ccc tgc Ala Ile Leu Lys Cys Asn Asn Lys Thr Phe Asn Gly Thr Gly Pro Cys 195 200 205	624
acc aac gtg agc acc gtg cag tgc acc cag gga att cgc ccc gtg gtg Thr Asn Val Ser Thr Val Gln Cys Thr His Gly Ile Arg Pro Val Val 210 215 220	672
agc acc cag ctg ctg ctg aac gcc agc ctg gcc gag gag gag gtg gtg Ser Thr Gln Leu Leu Leu Asn Gly Ser Leu Ala Gln Glu Glu Val Val 225 230 235 240	720
atc aga tct gag aac ttc acc aac aac gcc aag acc atc atc gtg cag Ile Arg Ser Glu Asn Phe Thr Asn Asn Ala Lys Thr Ile Ile Val Gln 245 250 255	768
ctg aac gag agc gtg gag atc aac tgc acc cgc ccc aac aac aac acc Leu Asn Glu Ser Val Glu Ile Asn Cys Thr Arg Pro Asn Asn Asn Thr 260 265 270	816
cgc aag agc atc cac atc gcc cct gcc cgc gcc ttc tac acc acc gcc Arg Lys Ser Ile His Ile Gly Pro Gly Arg Ala Phe Tyr Thr Thr Gly 275 280 285	864
gac atc atc gcc gac atc cgc cag gcc cac tgc aac atc tct aga acc Asp Ile Ile Gly Asp Ile Arg Gln Ala His Cys Asn Ile Ser Arg Thr 290 295 300	912

aac tgg acc aac acc ctg aag cgc gtg gcc gag aag ctg cgc gag aag 960
 Asn Trp Thr Asn Thr Leu Lys Arg Val Ala Glu Lys Leu Arg Glu Lys
 305 310 315 320

ttc aac aac acc acc atc gtg ttc aac cag agc tcc gcc ggc gac ccc 1008
 Phe Asn Asn Thr Thr Ile Val Phe Asn Gln Ser Ser Gly Gly Asp Pro
 325 330 335

gag atc gtg atg cac agc ttc aac tgc gcc gcc gag ttc ttc tac tgc 1056
 Glu Ile Val Met His Ser Phe Asn Cys Gly Gly Glu Phe Phe Tyr Cys
 340 345 350

aac acc acc cag ctg ttc aac agc acc tgg aac gag acc aac agc gag 1104
 Asn Thr Thr Gln Leu Phe Asn Ser Thr Trp Asn Glu Thr Asn Ser Glu
 355 360 365

gcc aac atc act agt gcc acc atc acc ctg ccc tgc cgc atc aag cag 1152
 Gly Asn Ile Thr Ser Gly Thr Ile Thr Leu Pro Cys Arg Ile Lys Gln
 370 375 380

atc att aac atg tgg cag gag gtg gcc aag gcc atg tac gcc ccc ccc 1200
 Ile Ile Asn Met Trp Gln Glu Val Gly Lys Ala Met Tyr Ala Pro Pro
 385 390 395 400

atc gcc gcc cag atc aag tgc ctg agc aac atc acc gcc ctg ctg ctg 1248
 Ile Gly Gly Gln Ile Lys Cys Leu Ser Asn Ile Thr Gly Leu Leu Leu
 405 410 415

acc cgc gac gcc gcc agc gac aac tgc agc agc gcc aag gag att ttc 1296
 Thr Arg Asp Gly Gly Ser Asp Asn Ser Ser Ser Gly Lys Glu Ile Phe
 420 425 430

cgc ccc gcc gcc gcc gac atg cgc gac aac tgg cgc agc gag ctg tac 1344
 Arg Pro Gly Gly Gly Asp Met Arg Asp Asn Trp Arg Ser Glu Leu Tyr
 435 440 445

aag tac aag gtg gtg aag atc gag ccc ctg gcc atc gcc ccc acc aag 1392
 Lys Tyr Lys Val Val Lys Ile Glu Pro Leu Gly Ile Ala Pro Thr Lys
 450 455 460

gcc aag cgc cgc gtg gtg cag cgc gag aag cgc gcc tag 1431
 Ala Lys Arg Arg Val Val Gln Arg Glu Lys Arg Ala *
 465 470 475

210: 74

211: 476

212: FRT

213: Artificial Sequence

400: 74

Ala Ser Ala Ala Asp Arg Leu Trp Val Thr Val Tyr Tyr Gly Val Pro
 1 5 10 15
 Val Trp Lys Asp Ala Thr Thr Thr Leu Phe Cys Ala Ser Asp Ala Lys
 20 25 30
 Ala Tyr Asp Thr Glu Val His Asn Val Trp Ala Thr His Ala Cys Val
 35 40 45
 Pro Thr Asp Pro Asn Pro Gln Glu Val Val Leu Gly Asn Val Thr Glu

30	55	60
Asn Phe Asn Met Gly Lys Asn Asn Met Val Glu Gln Met His Glu Asp		
65	70	75
Ile Ile Ser Leu Trp Asp Gln Ser Leu Lys Pro Cys Val Lys Leu Thr		80
	85	90
Pro Leu Cys Val Thr Leu Asn Lys Thr Lys Leu Lys Asn Ser Thr Asp		95
	100	105
Thr Asn Asn Thr Arg Trp Gly Thr Gln Glu Met Lys Asn Cys Ser Phe		110
	115	120
Asn Ile Ser Thr Ser Val Arg Asn Lys Met Lys Arg Glu Tyr Ala Leu		125
	130	135
Phe Tyr Ser Leu Asp Ile Val Pro Ile Asp Asn Asp Asn Thr Ser Tyr		140
445	150	155
Arg Leu Arg Ser Cys Asn Thr Ser Ile Ile Thr Gln Ala Cys Pro Lys		160
	165	170
Val Ser Phe Glu Pro Ile Pro Ile His Phe Cys Ala Pro Ala Gly Phe		175
	180	185
Ala Ile Leu Lys Cys Asn Asn Lys Thr Phe Asn Gly Thr Gly Pro Cys		190
	195	200
Thr Asn Val Ser Thr Val Gln Cys Thr His Gly Ile Arg Pro Val Val		205
	210	215
Ser Thr Gln Leu Leu Leu Asn Gly Ser Leu Ala Glu Glu Glu Val Val		220
225	230	235
Ile Arg Ser Glu Asn Phe Thr Asn Asn Ala Lys Thr Ile Ile Val Gln		240
	245	250
Leu Asn Glu Ser Val Glu Ile Asn Cys Thr Arg Pro Asn Asn Asn Thr		255
	260	265
Arg Lys Ser Ile His Ile Gly Pro Gly Arg Ala Phe Tyr Thr Thr Gly		270
	275	280
Asp Ile Ile Gly Asp Ile Arg Gln Ala His Cys Asn Ile Ser Arg Thr		285
	290	295
Asn Trp Thr Asn Thr Leu Lys Arg Val Ala Glu Lys Leu Arg Glu Lys		300
305	310	315
Phe Asn Asn Thr Thr Ile Val Phe Asn Gln Ser Ser Gly Gly Asp Pro		320
	325	330
Glu Ile Val Met His Ser Phe Asn Cys Gly Gly Glu Phe Phe Tyr Cys		335
	340	345
Asn Thr Thr Gln Leu Phe Asn Ser Thr Trp Asn Glu Thr Asn Ser Gln		350
	355	360
Gly Asn Ile Thr Ser Gly Thr Ile Thr Leu Pro Cys Arg Ile Lys Gln		365
	370	375
Ile Ile Asn Met Trp Gln Glu Val Gly Lys Ala Met Tyr Ala Pro Pro		380
385	390	395
Ile Gly Gly Gln Ile Lys Cys Leu Ser Asn Ile Thr Gly Leu Leu Leu		400
	405	410
Thr Arg Asp Gly Gly Ser Asp Asn Ser Ser Ser Gly Lys Glu Ile Phe		415
	420	425
Arg Pro Gly Gly Gly Asp Met Arg Asp Asn Trp Arg Ser Glu Leu Tyr		430
	435	440
Lys Tyr Lys Val Val Lys Ile Glu Pro Leu Gly Ile Ala Pro Thr Lys		445
	450	455
Ala Lys Arg Arg Val Val Gln Arg Glu Lys Arg Ala		460
465	470	475

<210> 75

<211> 1038

<212> DNA

<213> Artificial Sequence

<220>
 <211> CDS
 <222> (1)...(1038)

<400> 75

ggc gtg ggc atc ggc gct atg ttc ctc ggc ttc ctg ggc gct gca ggc	48
Ala Val Gly Ile Gly Ala Met Phe Leu Gly Phe Leu Gly Ala Ala Gly	
1 5 10 15	
agg acc atg ggc gcc gcc agc ctg acc ctg acc gtg cag gcc cgc cag	96
Ser Thr Met Gly Ala Ala Ser Leu Thr Leu Thr Val Gln Ala Arg Gln	
20 25 30	
ctg ctg agc ggc atc gtg cag cag cag aac aac ctg ctg cgc gcc atc	144
Leu Leu Ser Gly Ile Val Gln Gln Gln Asn Asn Leu Leu Arg Ala Ile	
35 40 45	
gag gcc cag cag cac ctg ctc cag ctg acc gtg tgg ggc atc aag cag	192
Glu Ala Gln Gln His Leu Leu Gln Leu Thr Val Trp Gly Ile Lys Gln	
50 55 60	
ctc cag gcc cgc gtg ctg gct cta gag cgc tac ctc cag gac cag cgc	240
Leu Gln Ala Arg Val Leu Ala Leu Glu Arg Tyr Leu Gln Asp Gln Arg	
65 70 75 80	
ttc ctg ggc atg tgg ggc tgc tcc ggc aag ctg atc tgc acc acg gcc	288
Phe Leu Gly Met Trp Gly Cys Ser Gly Lys Leu Ile Cys Thr Thr Ala	
85 90 95	
gtg ccc tgg aac gcc agc tgg agc aac aag aac ctg agc cag att tgg	336
Val Pro Trp Asn Ala Ser Trp Ser Asn Lys Asn Leu Ser Gln Ile Trp	
100 105 110	
gac aac atg acc tgg atg gag tgg gag cgc gag atc agc aac tac acc	384
Asp Asn Met Thr Trp Met Glu Trp Glu Arg Glu Ile Ser Asn Tyr Thr	
115 120 125	
gag atc atc tac agc ctg atc gag gag agc cag aac cag cag gag aag	432
Glu Ile Ile Tyr Ser Leu Ile Glu Glu Ser Gln Asn Gln Gln Glu Lys	
130 135 140	
aac gag ctg gac ctg ctc cag ctg gac aag tgg gca agc ttg tgg aac	480
Asn Glu Leu Asp Leu Leu Gln Leu Asp Lys Trp Ala Ser Leu Trp Asn	
145 150 155 160	
tgg ttc aac atc acc aac tgg ctg tgg tac atc aag att ttc atc atg	528
Trp Phe Asn Ile Thr Asn Trp Leu Trp Tyr Ile Lys Ile Phe Ile Met	
165 170 175	
atc gtg ggc ggc ctg atc ggc ctg cgc atc gtg ttc acc gtg ctg agc	576
Ile Val Gly Gly Leu Ile Gly Leu Arg Ile Val Phe Thr Val Leu Ser	
180 185 190	
atc gtg aac cgc gtg cgc cag ggc tac agc ccc ctg agc ttc cag acc	624
Ile Val Asn Arg Val Arg Gln Gly Tyr Ser Pro Leu Ser Phe Gln Thr	
195 200 205	
cgc ctg ccc gtg ccc cgc ggc ccc gac cgc ccc gag ggc atc gag gag	672
Arg Leu Pro Val Pro Arg Gly Pro Asp Arg Pro Glu Gly Ile Glu Glu	

210	215	220	
gag ggc ggc gag cgc gac cgc gac cgc agc acc cgc ctg gtg acc ggc			720
Glu Gly Gly Glu Arg Asp Arg Asp Arg Ser Thr Arg Leu Val Thr Gly			
225	230	235	240
ttc ctg ccc ctg atc tgg gac gac ctg cgc agc ctg ttc ctg ttc agc			768
Phe Leu Pro Leu Ile Trp Asp Asp Leu Arg Ser Leu Phe Leu Phe Ser			
245	250	255	
tac cat cga ttg cgc gac ctg ctg ctg atc gtg gcc cgc atc gtg gag			816
Tyr His Arg Leu Arg Asp Leu Leu Leu Ile Val Ala Arg Ile Val Glu			
260	265	270	
ctg ctg ggc cgc cgc ggc tgg gag atc ctg aag tac tgg tgg aac ctg			864
Leu Leu Gly Arg Arg Gly Trp Glu Ile Leu Lys Tyr Trp Trp Asn Leu			
275	280	285	
ctc cag tac tgg agc cag gag ctg aag aac tct gca gtg agc ctg ctg			912
Leu Gln Tyr Trp Ser Gln Glu Leu Lys Asn Ser Ala Val Ser Leu Leu			
290	295	300	
aac gcc acc gcc atc gcc gtg gcc gag gcc acc gac cgc gtg atc gag			960
Asn Ala Thr Ala Ile Ala Val Ala Glu Gly Thr Asp Arg Val Ile Glu			
305	310	315	320
gtg gtg cag cgc atc tgg cgc ggc atc ctg cac atc ccc acc cga att			1008
Val Val Gln Arg Ile Trp Arg Gly Ile Leu His Ile Pro Thr Arg Ile			
325	330	335	
cgc cag gcc ttc gag cgc gcc ctg ctg taa			1038
Arg Gln Gly Phe Glu Arg Ala Leu Leu *			
340	345		

<210> 76

<211> 345

<212> PRT

<213> Artificial Sequence

<400> 76

Ala Val Gly Ile Gly Ala Met Phe Leu Gly Phe Leu Gly Ala Ala Gly			
1	5	10	15
Ser Thr Met Gly Ala Ala Ser Leu Thr Leu Thr Val Gln Ala Arg Gln			
20	25	30	
Leu Leu Ser Gly Ile Val Gln Gln Asn Asn Leu Leu Arg Ala Ile			
35	40	45	
Glu Ala Gln Gln His Leu Leu Gln Leu Thr Val Trp Gly Ile Lys Gln			
50	55	60	
Leu Gln Ala Arg Val Leu Ala Leu Glu Arg Tyr Leu Gln Asp Gln Arg			
65	70	75	80
Phe Leu Gly Met Trp Gly Cys Ser Gly Lys Leu Ile Cys Thr Thr Ala			
85	90	95	
Val Pro Trp Asn Ala Ser Trp Ser Asn Lys Asn Leu Ser Gln Ile Trp			
100	105	110	
Asp Asn Met Thr Trp Met Glu Trp Glu Arg Glu Ile Ser Asn Tyr Thr			
115	120	125	
Glu Ile Ile Tyr Ser Leu Ile Glu Glu Ser Gln Asn Gln Gln Glu Lys			
130	135	140	

Asn	Glu	Leu	Asp	Leu	Leu	Gln	Leu	Asp	Lys	Trp	Ala	Ser	Leu	Trp	Asn
145					150					155					160
Trp	Phe	Asn	Ile	Thr	Asn	Trp	Leu	Trp	Tyr	Ile	Lys	Ile	Phe	Ile	Met
			165						170						175
Ile	Val	Gly	Gly	Leu	Ile	Gly	Leu	Arg	Ile	Val	Phe	Thr	Val	Leu	Ser
			180					185						190	
Ile	Val	Asn	Arg	Val	Arg	Gln	Gly	Tyr	Ser	Pro	Leu	Ser	Phe	Gln	Thr
		195					200					205			
Arg	Leu	Pro	Val	Pro	Arg	Gly	Pro	Asp	Arg	Pro	Glu	Gly	Ile	Glu	Glu
		210				215					220				
Glu	Gly	Gly	Glu	Arg	Asp	Arg	Asp	Arg	Ser	Thr	Arg	Leu	Val	Thr	Gly
225					230					235					240
Phe	Leu	Pro	Leu	Ile	Trp	Asp	Asp	Leu	Arg	Ser	Leu	Phe	Leu	Phe	Ser
				245					250						255
Tyr	His	Arg	Leu	Arg	Asp	Leu	Leu	Leu	Ile	Val	Ala	Arg	Ile	Val	Glu
			260						265					270	
Leu	Leu	Gly	Arg	Arg	Gly	Trp	Glu	Ile	Leu	Lys	Tyr	Trp	Trp	Asn	Leu
		275					280						285		
Leu	Gln	Tyr	Trp	Ser	Gln	Glu	Leu	Lys	Asn	Ser	Ala	Val	Ser	Leu	Leu
		290				295					300				
Asn	Ala	Thr	Ala	Ile	Ala	Val	Ala	Glu	Gly	Thr	Asp	Arg	Val	Ile	Glu
305					310					315					320
Val	Val	Gln	Arg	Ile	Trp	Arg	Gly	Ile	Leu	His	Ile	Pro	Thr	Arg	Ile
				325					330					335	
Arg	Gln	Gly	Phe	Glu	Arg	Ala	Leu	Leu							
			340					345							